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                   GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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protein NPR1 (NPR1) mRNA, complete
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;

Sosidae; eurosida II; Brassicales; Brassicaceae; Arabidopsis.

(Dases 1 to 2104)

Cao, H., Glazebrook, J., Clarke, J.D., Volko, S. and Dong, X.

The Arabidopsis NPRI gene that controls systemic acquired resistance encodes a novel protein containing ankyrin repeats

Call 88 (1), 57-63 (1997)
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   ATU76707 2104 bp
Arabidopsis thaliana regulatory
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RDAVDFMLEVLILKEPITALDDACALHFAVAYCSNVTATPDLLKLDLEDVHNTRALDS
DDTELVKLLLKEPITALDDACALHFAVAYCNVTATPLLKLGLEDVHNTRALDS
DDTELVKLLLEDEDVRTGASASEATLGGFATAMIARQATMAVECNNTPEQCKHSLKGR
LCVETLEQEDKREQIPROPPSSFAVAADELKWTLLDLENRYALAQATMAT
LCVETLEQEDKREQIPROPPSSFAVAADELKWTLLDLENRYALAGREFFF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (08-AUG-2001) Salk Institute Genomic Analysis Laboratory (SIGnAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

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ALQLLSNSFESYFDSPDDFYSDAKLVLSDGREVSFHRCVLARSSFFKSALAAAKKEK
BONTAAVKLELKEIAKDFYSTBYGFDSVYVLALAYVS SSRVRPPRGVSECADBNCCHVAC
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LLDRCKEIIVKSNVDMVSLEKSLPEELVKEIIDRRKELGLEVPKVKKHVSNVHKALDS
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VAANKKEPOLILISILEKGAGASEATLEGRTALMIAKOATMAVECNNIPPEOCRHSIKGR
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AEMKGTCEFTYSLEEPPRIJGTRRISPGVKIAPFRILEEHOSKIKALSKTVEIGKREF
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                                                                                                                        The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL CDNAS: Koesema,E., Chen,H., Cheuk,R., Kim,C.J., Meyers,M.C., Shinn, P., Banh,J. Bowser,L., Dale,J.M., Goldsmith,A.D., Jiang,P.X., Jones,T., Karlin-Neumann,G. Lam,B., Lee,J.M., Lin,J., Liu,S.X., Miranda,M., Nguyen,M., Ondera,C.S., Palm,C.J., Pham,P.K., Quach,H.L., Southwick,A., Pang,C.C., Toriumi,M., Yamada,K., Yamamura, Y., Yu,G., Yu,S., Davis,R.W., Theologis,A., and Ecker,J.R.
collection and clustering of RAFL cDNAS (RAFL cDNA : 'RIKEN Arabidopsis Full-Length cDNA') : Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                                                                       Koesema, E. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk) contributed equally to this work as PIs.

Location/Qualifiers
1. 2154
/organism="Arabidopsis thaliana"
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/note="transcription factor inhibitor I kappa
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/chromosome="l"
/clone="RAFL07-16 K16(R13446)"
/note="ecotype: Columbia"
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/protein_id-"AAK91469.1"
/db_xref-"GI:15215850"
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Uknes,S.Joseph, Hunt,M.Denise, Steiner,H. and Ryals,J.Andrew.
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                                                                                                                                                                     PLN 19-JAN-2001
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Lin X., Kaul, S., Town, C.D., Benito, M. I., Creasy, T. H., Haas, B.J.,

Wu, D., Maiti, R., Ronning, C.M., Koo, H., Fujii, C.Y., Utterback, T. R.,

Barnstead, M.E., Bowman, C.L., White, O., Nierman, W.C. and Fraser, C.M.

Arabidopsis, thaliana chromosome 1 BAC F15H21 genomic sequence
                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (25-APR-2000) The Institute for Genomic Research, 9712 Medical Center Dr. Rockville, MD 20850, USA, xlinetigr.org 3 (bases 1 to 96887)

Town, C.D. and Kaul, S.
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                                                                                                                                                          AC066689 96887 bp DNA linear PLN 19-JAN Arabidopsis thaliana chromosome 1 BAC F15H21 genomic sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission Submission Submitted (19-JAN-2001) The Institute for Genomic Research, 9 Medical Center Dr. Rockville, MD 20850, USA, cdtcwn@tigr.org On Jan 19, 2001 this sequence version replaced gi:12280769. Address all correspondence to:at@tigr.org
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/db_xref="taxon:3702"
/chromosome="1"
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/gene="F15H21.17"
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<887. .>1915
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Lin, X. and Kaul, S.
Direct Submission
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/rpt_family="SIMPLEGUY1|SIMPLEGUY1 sIMPLEGUY1 is a putative non-autonomous DNA transposon - a consensus." complement(join(<4109. .4202,4301. .4392,4524. .4606, 4711. .4789,5171. .5398,5484. .5585,5691. .5826,6091. .6140,
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                                                                                                                                        DPKISVNAVQLPSFAVSNNTANFSESOYVAVRNPNRATESHYDSSIQLLYSGNOVGEN
FIPAGKIDSGRIQYMAATFTVHSFPISPSSSAISTVSAAVIDDSPIIPGPPDFTVTP
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SPFFINPPRNPGAPVIPRNPNPPVFPGNPGRPSFPRNPGSPEFPGNFGAPIIPRNPG
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GSVLGFHC"
/product-"hypothetical protein; 887-1915"

*Protein_ad="AAG5175.1"

*db_xref="G1:1323476"

/translation="MAKPHDRRRSSGRTNLASCAVATVFLLILLVVLLVVYFTVFKPK
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/rpt_family="SIMPLEGUY1|SIMPLEGUY1 is a putative non-autonomous DNA transposon - a consensus." complement (3384. .3494)

/rpt_family="SIMPLEGUY1|SIMPLEGUY1 SIMPLEGUY1 is a putative non-autonomous DNA transposon - a consensus." complement (3384. .3457)

/rpt_family="SIMPLEGUY1|SIMPLEGUY1 is a consensus." /rpt_family="SIMPLEGUY1|SIMPLEGUY1 is a putative non-autonomous DNA transposon - a consensus."
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/rpt_family="SIMPLEGUY1|SIMPLEGUY1 is a putative non-autonomous DNA transposon - a consensus." complement(3196. .3285)
/rpt_family="SIMPLEGUY1|SIMPLEGUY1 is a putative non-autonomous DNA transposon - a consensus."
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/rpt_family="SIMPLEGUY1|SIMPLEGUY1 is a
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putative non-autonomous DNA transposon - a consensus."
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/rpt_family="SIMPLEGUY1|SIMPLEGUY1 is a
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/rpt_family="SIMPLEGUY1|SIMPLEGUY1 is a
putative non-autonomous DNA transposon - a consensus.
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/rpt_family="SIMPLEGUY1|SIMPLEGUY1 is a putative non-autonomous DNA transposon - a consensus.
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/rpt_family="SIMPLEGUY1|SIMPLEGUY1 is a putative non-autonomous DNA transposon - a consensu
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/rpt_family="SIMPLEGUY1|SIMPLEGUY1 is
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/rpt_family="SIMPLEGUY1|SIMPLEGUY1 is
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/note="e1m"
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complement(4109.
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6390. .>6572))
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/gene="Fi5H21.10"

complement (6810. .10294)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     join(11471. .11617,11714. .11766,12058. .12191,12213. .12309,
12686. .12786,13367. .13702,13835. .13925,14904. .15298,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(join(7338. 7400,7552. 7605,7688. 7759, 7853. 7940,8028. 8095,8180. 8287,8409. 8792,9058. .9106,9145. .9224,9310. .9387,9478. .9629,9686. .10133))
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                                                                                                                            /translation="wygnilvtggagyigshtvlolliggyntvidnldnsslvsig
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STONMENDALOGALKPKSVAKATOOOLUS TVDTENEVNIKVNIMELKXIKNNOOPRESSNK
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SNNPFGYGSSPNST"
                                                   putative; 6572-4109
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12686. .12786,13367. .13702,13835. .13925,14904. .15298.
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0; Mismatches
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Matches 2088; Conserv
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                                                                                                                                     TCTTCAAGAGCGCTTTTAGCCGCCGCTAAGAAGGAGAAAAGACTCCAACAACAACACCGCCG
                                                                                                                                                                                                                                                              88835 ACCATCTGCATTAAGCTATGGTTACACATTCATGAATATGTTCTTACTTGAGTACTTGTA
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ATTCTTATGAAATCAGCAGCACTAGTTTCGTCGCTACCGATAACACCGACTCCTATTG
                                                                                                                                                                                                                                                                                                             TGAAGCTCGAGCTTAAGGAGATTGCCAAGGATTACGAAGTCGGTTTCGATTCGGTTGTGA
                                                                                                                       CCAACAGCTTCGAATCCGTCTTTGACTCGCCGGATGATTTCTACAGCGACGCTAAGCTTG
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Db 90455 GCATCCTGTGTATTATTGCTGCAGGTGTGCTTCAAAC.  OY 2044 ATGCTATACAGATTTGTAATATATATTATGTACATC.  Db 90515 ATGGTATACAGATTTGTAATATATTATGTACATC.	RESULT 6 AR087501 LOCUS LOCUS DEFINITION Sequence 1 from patent US 5986082. ACCESSION AR087501 VERSION AR087501 KRYMORPIS	Unknown. SM Unknown. Unclassified. E 1 (bases 1 to 5655) S Uknes, S.Joseph, Hunt, M.Denise, Ste Altered forms of the NIMI gene con plants	JOURNAL Patent: US 5986082-A 1 16 NOV-1999; FEATURES Location/Qualifiers 15655 BASE COUNT 1758 a 1014 c 1069 g 1814 to ORIGIN	Query Match 83.7%; Score 1760; I Best Local Similarity 87.5%; Pred. No. 0; Matches 2088; Conservative 0; Mismatches Qy I TCGATCTTTACCAARCCAATCCAGTTGATAGGTCTTTCC	Db 2695 TCGATCTTTAACCAAATCCAGTTGATAAGGTCTCTTCC  Qy 61 ATTTGTGAATTTCAATTCATCGGAACCTGTTGATGGAC  Db 2755 ATTTGTGAATTTCAATTCATCGGAACCTGTTGATGGAC	QY 121 ATTCTTATGAAATCAGCAGCACTAGTTTCGTGGCTACC	Db 2875 TTTATCTGGCGCCGAACAAGTACTCACCGGACCTGAI Qy 241 CCAACAGCTTCGAATCCGTCTTTGACTCGCGGATGAI Db 2935 CCAACAGCTTCGAATCCGTCTTTGACTCGCCGGATGAI Qy 301 TTCTCCGACGGCCGGAAGTTTCTTTCACCGGTGT	Db 2995 TTCTCTCCGACGGGAAGTTTCTTTCCACGGTGC Qy 361 TCTTCAAGAGGCTTTAGCCGCGCGTAAGAAGAAAA Db 3055 TCTTCAAGAGCGCTTTAGCCGCCGCTAAGAAGAGAAAA Qy 421 TGAAGCTCGACCTTAAGGAGATTGCCAAGGATTACGAA		Db 3235 GCGCAGACGAGATTCCTGCCACGTGCCTTGCCGGCCG
	QY         1242         CAATGCAAGCATTCTCTCAAAGGCCGACTATGTGTAGAAATACTAGAGCAAGAAGACAAA         1301           B         111111111111111111111111111111111111			ω ω		Db 89975 CATCGGACTCCTTATCACAAAAACTAAATGATCTTTAAACATGGTTTTGTTACT 90034  Qy 1593GTGGAACTCGGGAAACGATCTTCCGGGCT 1623  Db 90035 TGCTGTCTGACCTTGTTTTTTATCATCATGAACGGAAACGATTCTTCCCGCGCT 00004	TGAACTGTGGGACTTGACTCAACTGGCTTGCGGG TGAACTGTGAGGCTTGACTCAACTGGCTTGCGGG TGAACTGTGAGGACTTGACTCAACTGGCTTGCGGG TACAAAAGAAGGAAAGGTACAAGAGA TACAAAAAAAGAAGGTACATGGAAATACAAGAGA			
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ACAAATGTTGTAACAATTTGAACCA 90514
                                                                                                                                  tiner, H. and Ryals, J. Andrew. ferring disease resistance in
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                                                                                                                                                                                                           DB 6; Length 5655;
                                                                 linear
                      CAACAATAA 2088
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		Db 4 Qy 1 Db 4 Qy 1 Qy 1	4375 CGTCTCACTGG 1554 GAAGACCATCAA             4435 GAAGAGCATCAA 1593
			1593
		Db 4	4555 TGCTGTCTGAC 1623 TGTTCGGCAGT
762 AAKAGATTATTGTCAAGTCTAATGTAAATTATGGTTAATCTTGAAAAATCATTGCCGGAA 		oy d	4615 TGTTCGCCAGT 1683 GAAGACGACAC
822 GAGCTTGTTAAAGAGATAATTGATAGACGTAAAGAGCTTGGTTTGGAGGTACCTAAAGTA 1	AAAGTA 881          AAAGTA 3654	q	
882 AAGAAACATGTCTCGAATGTACATAAGGCACTTGACTCGGATGATATTGAGTTAGTCAAG 	GTCAAG 941         GTCAAG 3714		
942 TTGCTTTTGAAAGAGGATCACACCAATCTAGATGATGCGTGTGCTCTTCATTTCGCTGTT	GCTGTT 1001         GCTGTT 3774		4795 TCGACTTCTTC
1002 GCATATTGCAATGTGAAGACCGCAACAGATCTTTTAAAACTTGATCTTGCCGATGTCAAC 			4855 CGTCGTCGGTG
1062 CATAGGAATCCGAGGGATALACGGTGCTTCATGTTGCTGCGATGCGGAAGGAGCACACAA	GCACAA 1121  - - - -  GCACAA 3894		
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1182 ACCGCACTCATGATCGCAAAACAAGCCACTATGGCGGTTGAATGTAATAATATCCCGGAG 	CCCGGAG 1241          CCCGGAG 4014		5035 AATGGTATACA
1242 CAAIGCAAGCATICICCCAAAGGCCGACTAIGIGTAGAAATACTAGAGCAAGAAGAAAAAAAAAA	KGACAAA 1301         	RESULT 7 ATU87794 LOCUS DEFINITION	z
1302 CGAGAACAAATTCCTAGAGATGTTCCTCCTCTTTTGCAGTGGCGGCCGATGAATTGAAG	TTGAAG 1361         TTGAAG 4134	ACCESSION VERSION KEYWORDS	
1362 ATGACGCTGCTCGATCTTGAAAATAG	1387 .TGTTTG 4194	SOURCE ORGANI	SM
1388	1387	2222	Spermacok Rosidae; FNCF 1 (bases
4195 AATTAAATTTATGTCCTCTCTATTAGGAAACTGAGTGAACTAATGATAACTATTCTTTGT	CTTTGT 4254	AUTHORS	
1388AGTIGCACTIGCTCAACGTCTTTTCCAACGGAAGCACAAGCTGCA	GCTGCA 1433         CTGCA 4314	TITLE	
1434 ATGGAGATCGCCGAAATGAAGGGAACATGTGAGTTCATAGTGACTAGCCTCGAGCCTGAC 	GCCTGAC 1493           GCCTGAC 4374	JOUKNAL MEDLINE REFERENCE AUTHORS	KNAL PIANT CELLINE 97246324 ENCE 2 (bases RYAls,J.,
1494 CGTCTCACTGGTACGAAGAACATCACCGGGTGTAAAGATAGCACCTTTCAGAATCCTA	GAATCCTA 1553 	TITLE	

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5655 bp DNA linear PLN 25-MAY-1997 is thaliana transcription factor inhibitor I kappa B niml) gene, complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGACTCTTGCCTCTTAGTGTAATTTTTGCTGTACCATATAATTCTGTTT 1922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ITATCACAAAAACAAAACTAAATGATCTTTAAACATGGTTTTGTTACT 4554
                                                                                                                                                                           SCTCGACCAGATTATGAACTGTGAGGACTTGACTCAACTGGCTTGCGGA 1682
                                                                                                                                                                                                                                      IACGAAGAGAACATCACCGGGTGTAAAGATAGCACCTTTCAGAATCCTA 4434
                                  s 1 to 5655)

Weymann, K., Lawton, K., Friedrich, L., Ellis, D.,
H.-Y., Johnson, J., Delaney, T.P., Jesse, T., Vos, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s 1 to 5655), Weymann, K., Lawton, K., Friedrich, L., Ellis, D., H.-Y., Johnson, J., Delaney, T.P., Jesse, T., Vos, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     idopsis NIM1 protein shows homology to the mammalian ption factor inhibitor I kappa B
11 9 (3), 425-439 (1997)
                                                                                                                                                            -------GTGGAACTCGGGAACGATTCTTCCCGCGC
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sis thaliana
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.4162,4271. .4474,4586.
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Submitted (29-JAN-1997) Fungicides,
Road, Research Triangle Park, NC 277
Location/Qualifiers
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Pred. No. 0;
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Best Local Similarity 87.5%;
Matches 2088; Conservative
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1001 1061 1121 3894 1181 3954 1241 4014 1301 4074 1361 4134 1387 1387 4254 3534 3654 3714 4194 ATGGAGATCGCCGAAATGAAGGGAACATGTGAGTTCATAGTGACTAGCCTCGAGCCTGAC 1493 3354 3594 3414 3474 649 761 821 881 941 701 -----AGTTGCACTTGCTCAACGTCTTTTTCCAACGGAAGCACAAAGCTGCA TTGATACTATCTCTATTGGAAAAAGGTGCAAGTGCATCAGAAGCAACTTTGGAAGGTAGA ACCGCACTCATGATCGCAAAACAAGCCACTATGGCGGTTGAATGTAATATATCCCGGAG CAATGCAAGCATTCTCTCAAAGGCCGACTATGTGTAGAAATACTAGAGCAAGAAGAAAA CGAGAACAAATTCCTAGAGATGTTCCTCCCTCTTTTGCAGTGGCGGCCGATGAATTGAAG ATGACGCTGCTCGATCTTGAAATAGAGGTATCTATCAAGTCTTATTTCTTATATGTTTG GCGCAGACGAGAATTGCTGCCACGTGGCTTGCCGGCCGCCGCGGTGATTTCATGTTGGAGG GTTATACTCAAGCTTGCTAATATATGTGGTAAAGCTTGTATGAAGCTATTGGATAGATGT AAGAAACATGTCTCGAATGTACATAAGGCACTTGACTCGGATGATATTGAGTTAGTCAAG TTGCTTTTGAAAGAGGATCACAATCTAGATGATGCGTGTGCTCTTCATTTCGCTGTT 3715 ITGCTITTGAAAGAGATCACACCAATCTAGATGATGCGTGTGCGTCTTCATTTCGCTGTT CATAGGAATCCGAGGGGATATACGGTGCTTCATGTTGCTGCGGATGCGGAAGGAGCCACAA TIGATACTATCTCTTTTGGAAAAGGTGCAAGTGCATCAGAAGCAACTTTGGAAGGTAGA GTCGTCCACTGTTAGTTGCACTTGCTCAACGTCTTTTTCCAACGGAAGCACAAGCTGCA ACCATCTGCATTAAGCTATGGTTACACATTCATGAATATGTTCTTACTTGAGTACTTGTA -----TCAGAGGCACTTATTGGACGTTGTAGACAAAGTTGTTATAGAGGACACATTG AAAGAGATTATTGTCAAGTCTAATGTAGATATGGTTAGTCTTGAAAAGTCATTGCCGGAA GAGCTTGTTAAAGAGATAATTGATAGACGTAAAGAGCTTGGTTTGGAGGTACCTAAAGTA GCATATTGCAATGTGAAGACCGCAACAGATCTTTTAAAACTTGATCTTGCCGATGTCAAC AATTAAATTTATGTCCTCTCTTTAGGAAACTGAGTGAACTAATGATAACTATTCTTTGT GTTATACTCAAGCTTGCTAATATATATGTGGTAAAGCTTGTATGAAGCTATTGGATAGATGT ATGACGCTCCTCTTGAAAATAG-----3295 3355 3475 ( 3535 822 3595 3655 1002 3775 1062 3835 1122 3895 1182 3955 1242 4015 1302 4075 1362 4135 4195 1434 3415 762 882 942 1388 4255 3235 1388 650 702 541 601 650 δλ

Force 1605; DB 6; Length 1608; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;	GATCTCTTTAATTTGTGAATTTCAATTCATCGGAACCTGTTGATGGACACCACCATTGAT 110 	GGATTCGCCGATTCTTATGAAATCAGCAGCACTAGTTTCGTCGCTACCGATAACACCGAC 170 	TCCTCTATTGTTATCTGGCCGCGAACAAGTACTCACCGGACCTGATGTATCTGCTCTG 230	CAATTGCTCTCCAACAGCTTCGAATCCGTCTTTGACTCGCCGGATGATTTCTACAGCGAC 290	GCTAAGCTTGTTCTCCCGACGGCCGGGAAGTTTCTTTCCACCGGTGCGTTTTGTCAGCG 350 	AGAAGCTCTTTCTTCAAGAGCGCTTTAGCCGCCTAAGAAGGAGAAAGACTCCAACAAC 410 	ACCGCCGCGTGAAGCTCGAGCTTAAGGAGATTGCCAAGGATTACGAAGTCGGTTTCGAT 470 	TCGGTTGTGACTGTTTTGGCTTATGTTTACAGCAGCAGAGTGAGACCGCCGCCTAAAGGA 530 	GTTTCTGAATGCGCAGAGAATTGCTGCCACGTGGCTTGCCGGCCG	atgitggaggitcictattitggcittcatcitcaagaicccigaattaattactcicat 650 	CAGAGCACTTATTGGACGTTGTAGACAAAGTTGTTATAGAGGACACATTGGTTATACTC 710 	aagcttgctaatatatgtggtaaagcttgtatgaagctattggatagatggaagatt 770 	attgtcaagtctaatgtagatatggttagtcttgaaaagtcattgccggaagagcttgtt 830 	AAAGAGATAATTGATAGACGTAAAGAGCTTGGTTTGGAGGTACCTAAAGTAAAGAAACAT 890 	GTCTCGAATGTACATAAGGCACTTGACTCGGATGATATTGAGTTAGTCAAGTTCCTTTTG 950 	AAAGAGGATCACACCAATCTAGATGATGAGTGTGCTCTTCATTTCGCTGTGCATATTGC 1010	GAAGACCGCAACAGATCTTTAAAACTTGATCTTGCCGATGTCAACCATAGGAAT 1070 	CCGAGGGGATATACGGTGCTTCATGTTGCTGCGGAAGGAGGAGCCACAATTGATACTA 1130
Query Match 76.3%; Sc Best Local Similarity 100.0%; P Matches 1605; Conservative 0;	Qy 51 GATCTCTTAATTTGTGAATTTCAAT	Qy 111 GGATTCGCCGATTCTTATGAAATCAG	Qy 171 TCCTCTATTGTTTATCGCGCCGCGA DD 121 TCCTCTATGTTTATCTGGCCGCCGA	Qy · 231 CAATTGCTCTCCAACAGCTTCGAATC	Qy 291 GCTAAGCTTGTTCTCCGACGGCCG	Oy 351 AGAAGCTCTTTCTTCAAGAGGGCTTT	Qy 411 ACGCCGCGTGAAGCTCGAGCTTAA 	Qy 471 TCGGTTGTGACTGTTTTGGCTTATGT	Oy 531 GTTCTGAATGCGCAGACGAGAATTC	Oy 591 ATGTTGGAGGTTCTCTATTTGGCTT	Oy 651 CAGAGGCACTTATTGGACGTTGTAG 	OY 711 AAGCTTGCTAATATATGTGGTAAAG 	OY 771 ATTGTCAAGTCTAATGTAGATATGG 	Oy 831 AAAGAGATAATTGATAGACGTAAAG 	Qy 891 GTCTCGAATGTACATAAGGCACTTG	Oy 951 AAAGAGGATCACAATCTAGATG	1011 AATGT       961 AATGT	1071
Db 4315 ATGGAGATCGCCGAAATGAAGGGAACATGATCATAGTGACTAGCCTCGAGCCTGAC 4374	QY 1494 CGTCTCACTGGTACGAAGAACATCACCGGGTGTAAAGATAGCACCTTTCAGAATCCTA 1553 D1494 CGTCTCACTGGTACGAAGAACATCACCGGGTGTAAAGATAGCACCTTTCAGAATCCTA 4434 A375 CGTCTCACTGGTACGAAGAACATCACCGGGTGTAAAGATAGCACCTTTCAGAATCCTA 4434	9 9	QY 1593 1592  Db 4495 CATCGGACTCCTTATCACAAAAACAAAACTAAATGATCTTTAAACATGGTTTTGTTACT 4554	OY 1593	OY 1623 TGTTCGGCAGTGCTCGACCATATGAACTGTGAGGACTTGACTCAACTGGCTTGCGA 1682  Db 4615 TGTTCGGCAGTGCTCGACCAGATTATGAACTGTGAGGACTTGACTCAACTGGCTTGCGGA 4674	OY 1683 GAAGACGACTGCTGAGAAACGACTACAAAAGCAAGCAAAGGTACATGGAAATACAAGAG 1742 	QY 1743 ACACTAAAGAAGGCCTTTAGTGAGGACAATTTGGAATTAGGAAATTCGTCCCTGACAGAT 1802	OY 1803 TCGACTTCTTCCACATCGAAATCAACCGTGGAAAGGTCTAACCGTAAACTCTCTCAT 1862 	OY 1863 CGTCGTCGGTGAGACTCTTGCCTCTAGTGTAATTTTGCTGTACCATATAATTCTGTT 1922	OY 1923 TCATGATCACTGTAACTGTTTATGTCTATCGTTGGCGTCATATAGTTTCGCTCTTCGTTT 1982	OY 1983 TGCATCCTGTATTATTGCTGCAGGTGTGCTTCAAACAAATGTTGTAACAATTTGAACC 2042	Qy 2043 AATGGTATACAGATTTGTAATATTTTATGTACATCAACAATAA 2088 	1608 b	ION Sequence 11 from patent US 5 ON AR087505 I AR087505.1 GI:10014268	Unknown. IM Unknown. Unclassified. 1 (bases 1 to 1608)	Uknes, S Altered plants	ratemic 0.5 9500002 h 11 to NV 1999 Location/Qualifiers 11608 /organism="unknown" .25	BASE COUNT 447 a 340 c 385 g 436 t ORIGIN

us-08-908-884-2.rge

1021   CCGARGGGGATATACGGGGGGGCGCGCGCGCCCCCCCCCC	1190 Db 122	1250 Db 182 T 1250 Oy 706 T	1310 Db 242 1360 Qy 766	1370 Db 302 1320 Qy 826	1430 Db 362 1430 Qy 886 1380	1490 Db 1440 QY	1550 Db 482 1500 Qy 1006	1610 Db 542 1560 Qy 1066	Db 602 GGAATCCG Qy 1126 TACTATCT Db 662 TACTATCT	07-SEP-2000 Db 722 QY 1246	1306	Db 842 AACAAATT Ob 842 CGCAGTGCTC Option	Db 902 CGCTGCTC  QY 1426 AAGCTGCA  Db 962 AAGCTGCA	.; Gans 0.	525 61	
	CCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	ATGATCGCAAAACCACCACTATGGCGGTTGAATGTAATAATATCCCGGAGCAATG 	CATTCTCTCAAAGGCCGACTATGTGTAGAAATACTAGAGCAAGAAGACAAAGA 		CTGGATCTTGAAAATAGAGTTGCACTTGCTCAACGTCTTTTTCCAACGAAGCACA 	GCAATGGAGATCGCCGAAATGAAGGGAACATGTGAGTTCATAGTGACTAGCCTCGA 	GACCGTCTCACTGGTACGAAGAGAACATCACCGGGTGTAAAGATAGCACCTTTCAG 	CTAGAAGAGCATCAAAGTAGACTAAAAGCGCTTTCTAAAACCGTGGAACTCGGGAA 	165	AR087504 1597 bp DNA linear Sequence 9 from patent US 5986082. AR087504.1 GI:10014267	_	<pre>1 (Dases 1 to 159/) Uknes,S.Joseph, Hunt,M.Denise, Steiner,H. Altered forms of the NIMl gene conferring plants</pre>	Patent: US 5986082-A 9 16-NOV-1999; Location/Qualifiers 1. 1597 /organism="unknown" 467 a 381 q 445	ch 75.7%; Score 1592.8; DB 6; Length a Similarity 99.9%; Pred. No. 0; Conservative 0; Mismatches 2: Indels	TCATTCGGTTGTGACTGTTTGGCTTATGTTTACAGCAGCAGCAGTGAGACCGCCG 	AAGGAGTITCTGAATGCGCAGAGAATTGCTGCCACGTGGCTTGCCGGCCG

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1666 CTCAACTGGCTTGCGGAGAAGACGACACTGCTGAGAAACGACTACAAAAGAAGCAAAGGT 1725

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TITLE	N Arabidopsis the project). AL049483. AL049483.1 GI.: thale cress. Arabidopsis the Eukaryota; viri Spermatophyta; Rosidae; eurosi I (bases 1 to Bevan, M., Rose, Mewes, H.W., May Unpublished 2 (bases 1 to	EU Arabidops Direct Submi Submitted (1 Biochemie, A Schuelle@mip Coordinator: Laboratory, E-mail: mich Information annotation viewed at: h	source 1104/38  /organism="Arabidopsis thaliana" /variety="Columbia" /db.xref="taxon:3702" /chromosome="4" exon 86261 /gene="F20B18.10" /mumber=1 /gene="F20B18.10" /gene="F20B18.10" /note="similarity to Pennisetum ciliare possible apospory-associated mRNA clone pSUB C, PID:9549984" /codon_start=1	/product="possible apospory-associated like protein(fragment)" /protein_id="changes" /pr	intron 5.65  fumber=2  exon / gene="F20B18.10"  / number=2  exon / gene="F20B18.10"  / number=3  for . 38  for . 38  / sene="F20B18.10"  / number=3  for . 386  / gene="F20B18.10"  / number=4  intron 897 1005  / number=4  exon 1006 1175
Altered forms of the NIMI gene conferring disease resistance in plants  Patent: US 5986082-A 15 16-NOV-1999;  Location/Qualifiers  1.786  Toroganism="unknown" and the plant of the plant of the plant of the plants	DEF VERY VERY SOU REF	ፈ E P C C A E P E P E P E P E P E P E P E P E P E			
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	Altered forms of the NIM1 gene conferring disease resistance plants Patent: US 5986082-A 15 16-NOV-1999; SS Location/Qualifiers J. 786 OUNT 221 a 136 c 200 g 229 t  Local Similarity 99.9%; Pred. No. 4.3e-191; Les 782; Conservative 0; Mismatches 1; Indels 0; Gaps JIMINITIES OF THE STANDS OF THE S	GTCGGTTTCGATTCGGTGGCGGCGGGGGGGGGGGGAGGGA	ATTACTCTCTATCAGAGGCACTTATTGGACGTTGTAGAGTTGTTATAGAGGACACA	GAAGACCTGTTAAAGAGATAATGATAGACGTAAAGAGCTTGGTTTGGAGGTACCTAAA [	AACCATAGGAATCCGAGGGATATACGGTGCTTCATGTTGCTGCGATGCGGAAGGACC

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ζζ,	1345	CGGCCGATGAATTGAAGATGACGCTGCTCGATCTTGAAAA
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ර් සි	1440 75728	ATCGCGAAATGAAGGGAACTGTGAGTTCATAATGATGACTCAGCCTCAGCGTCTC 1499 
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RE	REFERENCE AUTHORS	Roslade, eurosida Li, Brasstaales; Brasstaacee; Arabidopsi. 1 (bases 50686 to 155423; 144355 to 196286) Rose, M., Hempel, S., Entian, KD., Mewes, H.W., Lemcke, K. and
R	JOURNAL	
	AUTHORS	
REF	PERENCE	Unpublished 3 (bases 1 to 82307)
	AUTHORS	Peters, S.A., van Staveren, M., Dirkse, W., Stiekema, W., Mewes, H.W., Lemcke, K. and Mayer, K.F.X.
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TITLE AUTHORNA AUTHORNA TITLE JOURNA COMMENT  1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	CE 4 (bases 1 to 196286)  By Arabidopsis sequencing, project.  Direct Submission  AL Submission  Coordinator  Coordinator  Coordinator  Coordinator  Coordinator  Coordinator  Condinator  Condinator	FEATURES Location/Qualifiers  1. 196286 1. 196286   / Organism="Arabidopsis thaliana"   / Ab_xref="taxon:3702"   / Ab_xre	3, 34. 34. 34. 34. CPPA CVMV MGER DSLD DSLD HLAA HLAA	intron complement(68346919)  /gene="Ar4g25770" /number=1  exon complement(69207036) /gene="Ar4g25770" /number=2 intron /gene="Ar4g25770" /number=2 exon complement(70837163) exon complement(70837163)	

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Db 124928 CACCACCACCGCTAGATTCTCTGATTCATACGAGTTCAGCAACACAACAGCGGCAATAGCTT 124987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124988 CTTGGCGGCGGGTCATCTCTTGATTATCGACGG-----AATTTCTCACGCCACCGGA 125041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125102 GTTCTACAGCGATGCTAGAGTTACTCGCCGGCGCCGGGAGGTTTCTTTTACCGTTG 125161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125162 TATTCTTTCCGCGAGAATTCCTGTCTTCAAAAGCGCTTTAGCCACGTGAAGGAACAAAA 125221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125333 CCGCCGAAGGGAGCTTCTGCTTGCGTAGACGACGATGTTGTCCACGTGGCTTGCCGGTC 125392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  158 CGATAACACCGACTCCTCTATTGTTTATCTGGCCGCCGAACAAGTACTCACCGGACCTGA 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGTATCTGCTCTGCAATTGCTCTCCAACAGCTTCGAATCCGTCTTTGACTCGCCGGATGA 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   338 CGTTTTGTCAGCGAGAAGCTCTTTCTTCAAGAGCGCTTTAGCCGCCGCTAAGAAGGAGAA 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGACTCCAACAACACGCCGCCGTGAAGCTCGAGCTTAAGGAGATTGCCAAGGATTACGA 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98 CACCACCATTGATGGATTCGCCGATTCTTATGAAATCAGCAGCACTAGTTTCGTCGCTAC 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 196286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      282;
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Pred. No. 2.9e-166;
0; Mismatches 426;
                                                                                                                                                                                                                                                                                                                                                  /number=1
14239. .14669
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Best Local Similarity 64.8%;
Matches 1304; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               'number=2
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đ	125453	
QY	. 650	TCAGAGGCACTIATTGGACGTTGTAGACAAGTTGTTA 687
q	125513	TTAAGTCTCCTCTGTTTTCATTTCAGAGGCAGTTCTTGGAAATTGTAGACAAAGTTGTAG 125572
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QY Db	748	TATTGGATAGATGTAAAGAGATTATTGTCAAGTCTAATGTAGATATGGTTAGTCTTGAAA 807 
70 Y	80	29
<u>අ</u> :	12569	12
Å A	868 125753	AGGTACCTAAAGTAAAGAAACATGTCTCGAATGTACATAAGGCACTTGACTCGGATGATA 927 
QY	928	TTGAGTTAGTCAAGTTGCTTTTGAAAGAGGATCACACCAATCTAGATGATGCGTGTGCTC 987 
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QY Db	1108	GGAAGGAGCCACAATTGATACTATCTCTATTGGAAAAAGGTGCAAGTGCATCAGAAGCAA 1167 
9٧	126053	227
a	7.002	CALIGGAIGGIAGAACCGCITTAGIGAITGIAAAACGACICACTAAAAGCGGATGACTACA 126112
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Qy Db	1288	AGCAAGAAGACAAACGAGAACAAATTCCTAGAGATGTTCCTCCTCTTTTGCAGTGG 1344 
Ωy	1345	1384
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Qγ	1385	1384
g	126293	TCACTTGAATATCGAATTTCGGGTAGGAAAATGAGTGGAACTAATGATAACGATGGTCTA 126352
Qy Db	1385 126353	TAGAGTIGCACTIGCICAACGICTITITCCAACGGAAGCACAAGCIGCAAIGGAG 1439 
Qy	1440	ATGGCGGAAATGAAGGGAACATGTGAGTTCATAGTGACTGAGCCTGAGCGTGACCGTCT 1499 
ò	150	, G
d d	47	AUTOSTROMANDAMENTAL CANCEGO I PRANCATAN CANCELLI L'ANGANT CANANGA 1939 ATTGGTGAAAAGCGGACATCACTAGACCTAAATATGGCGCCGTTCCAAATCCATGAGAAG 126532
Ωy	1560	CATCAAAGTAGACTAAAAGCGCTTTCTAAAACC

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1684 AAGACGACACTGCTGAGAAACGACTACAAAAGAAGCAAAGGTACATGGAAATACAAGAGA 1743
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                                                                                                                                                                                                                                                                                                                                                                                                                                                1024 CAACAGATCTTTAAAACTTGATCTTGCCGATGTCAACCATAGGAATCCGAGGGGATATA 1083
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                                                                                                                                                                     GCCTCGGATTAATTTCACCAGAAACAAGGGATTTCCTAACAACATGTGAGGAGGATAC 337
                                                                                                                                                                                                                                                                                                ATAAGGCACTTGACTCGGATGATATTGAGTTAGTCAAGTTGCTTTTGAAAGAGGATCACA 963
                                                                                                                                                                                                                                                                                                                 995 TAGCTCGGATGACGCCACTCTCCAAAACAGTGGAGCTCGGGAAACGCTTTTTCCCGCGAT
                                                                                                                                                                                                                        AGCITGGITTGGAGGTACCTAAAGTAAAG-------AAACATGTCTCGAATGTAC
                                                                                                                                                                                                                                                                                                                                                                                             1324 TTCCTCCCTCTTTTGCAGTGGCGGCCGATGAATTGAAGATGACGCTGCTCGATCTTGAAA
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                                                                          CTTGTATGAAGCTATTGCATAGATGTAAAGAGATTATTGTCAAGTCTAATGTAGATATGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    818 ACCGAGITGCITTGGCGAGGATTATGTTTCCGATGGAGGCAAGAGTAGCAATGGATATTG
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HEDKEENDRSGLSSSSSTSIGAIRPRR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                      DD 126653 ACTGGGGAAACGCTACTTCAAACGATGTTC-----GCTTGATCACTTTATGGATACTGA 126706
                                                                                                                                                                                                                              126593 TCTTTTCTAGCCAACAAAGAAATGATGTTTAGAACTTTATTTTGTTGTATCTTCAGTGGA 126652
                                                                                                                                                                                                                                                                                                                                                          ATTAGGAAATTCGTCCCTGACAGATTCGACTTCTTCCACATCGAAATCAACCGGTGGAAA 1837
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                                                                                                                                                                                                                                                                                    GCAAAGGTACATGGAAATACAAGAGACACTAAAGAAGGCCTTTAGTGAGGACAATTTGGA 1777
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Monocotyledonous plant genes and uses thereof
Patent: WO 0166755-A 15 13-SEP-2001;
Syngenta Participations AG (CH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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Pred. No. 3.6e-82;
); Mismatches 486;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note-"unnamed protein product"
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Sequence 15 from Patent W00166755.
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Pooideae, Triticeae, Triticum.
1160 TICTTCAGAGGCATTCCACGAGGACAAGGAGAATGACAGGTCGGGGCTCTCGTCGT 1219
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                                           CGACTICTICCACATCGAAATCAACCGGTGGAAAGAGG 1841
                                                                     CGTCGTCATCGACATCGGGGCCATTCGACCAAGG 1257
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Pred. No. 2.6e-70;
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/db_xref="taxon:4565"
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Best Local Similarity 57.3%;
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                                                                                          CAATTGATACTATCTCTATTGGAAAAAGGTGCAAGTGCATCAGAAGCAACTTTGGAAGGT
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Copyright (c) 1993 - 2002 Compugen Ltd.
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Listing first 45 summaries
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/SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA197.DNT:\*
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/SIDSI/gcgdata/hold-geneseqy-embl/NA2001BDAT:\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. 14: 115: 117: 119: 220: 223: 23:

10:

SUMMARIES

Description	Arabidopsis thalia	A. thaliana NIM-1	A. thaliana NIM-1	Non-inducible immu	Arabidopsis thalia	A. thaliana NIM-1	A. thaliana non-in	Arabidopsis thalia	A. thaliana non-in
01	AAV16851	AAV46274	AAV46275	AAV43661	AAC37765	AAV46273	AAV43659	AAV04632	AAV43658
98	13	19	19	19	21	19	19	19	19
% Query Match Length DB	2104	2011	2011	2011	2024	5655	5655	5655	9919
% Query Match	100.0	95.5	95.4	95.4	94.8	83.7	83.7	83.7	83.7
Score	2104	2009.4	2006.2	2006.2	1993.6	1760	1760	1760	1760
Result No.	-	7	m	4	2	9	7	80	6 0

c 10	1760	83.7	9919	19	AAV04631 AAV16850	Arabidopsis thalia Arabidopsis thalia
12	160		1608	19	AAV46277	ď
13	1605		1608	19	AAV43663	]e
14	1592.8		1597	19	AAV46276	A. thaliana N-term
15	1592.8		1597	19	AAV43662	le i
16	1188.4		1194	19	AAV46278	thaliana C
17	1188.4		1194	19	AAV43664	
18	980.4		1740	21	AAA97192	
19	951.8		1803	21	AAA97202	. thaliana
20	951.8		1818	21		A. thaliana NIM1 h
21	781.4		786	19	AAV46279	A. thaliana NIM-1
22	781.4		786	19	AAV43665	ä
23	579		1731	21	AAA97191	
24	578.4		1767	21	AAA97190	N. tabacum NIM1 ho
25	578.4		2172	19	AAV16852	Nicotiana glutinos
56	554		2299	21	AAA97229	B. vulgaris NIM1 h
27	422.2		2040	22	AAC81457	Rice NPR1 homologu
28	419		2194	21	AAA61047	putative
29	360.4		1565	22	AAH43382	cDNA sequence enco
30	314.6		1668	22	AAH43384	Ž.
31	290.8		653	21	AAA97219	
32	288		629	21	AAA97211	
33	284.2		498	21	AAA97225	B. napus NIM1 homo
34	263.6		2673	21	AAA97234	N. tabacum NIM1 ho
35	260.2		2368	22	AAC84340	Rice Nph1 cDNA seq
36	258.6		1428	22	AAC84339	Rice Nph1 protein
37	258.6		2326	22	AAH43381	cDNA sequence enco
38	256.2		2069	21	AAA61048	Rice putative nega
39	241.6		4270	22	AAH43377	DNA sequence encod
40	233		498	21	AAA97215	L. esculentum NIM1
41	232.6		2154	21	AAC68800	ze NPR1 c
42	228.6		1761	21	~	
43	228.4		2171	21	~	Arabidopsis thalia
44	228.2		498	21	AAA97216	Z
45	225		2844	21		H.annuus NIM1 homo
					ALIGNMENTS	
RESULT 1						

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NPR1 gene; acquired resistance; disease; plant pathogens; bacteria; mycoplasma; fungi; insects; nematodes; viruses; viroids; transgenic; ds.
                                                                                                                                                             /product= acquired resistance protein
/note= NPR1 gene
                                                             Arabidopsis thaliana acquired resistance gene NPR1.
                                                                                                                                  Location/Qualifiers
93..1874
/*tag= a
        AAV16851 standard; cDNA; 2104 BP.
                                                                                                                                                                                                                                          97US-0046769.
96US-0023851.
97US-0035166.
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                                            (first entry)
                                                                                                                  Arabidopsis thaliana.
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09-AUG-1996;
10-JAN-1997;
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                                                                                                                                                                                                                                            ATTTGTGAATTTCAATTCATCGGAACCTGTTGATGGACACCACCATTGATGGATTCGCCG
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                                                      New isolated plant acquired resistance polypeptide gene - useful for, e.g. producing plants with increased resistance to pathogens such as bacteria
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Pred. No. 0;
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CTAATGTAGATATGGTTAGTCTTGAAAAGTCATTGCCGGAAGAGCTTGTTAAAGAGATAA
                                  ATATATGTGGTAAAGCTTGTATGAAGCTATTGGATAGATGTAAAGAGATTATTGTCAAGT
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2040
1741 AGACACTAAAGAAGGCCTTTAGTGAGGACAATTTGGAATTAGGAAATTCGTCCCTGACAG 1800
                                                                                                                                                     This cDNA sequence encodes the NIM-1 protein from Arabidopsis thaliana. This protein is used in a method resulting in the protection of an immunomodulated plant having a first level of resistance and involves treatment with at least 1 microbicide that confers a second level of
                                                                                                                                                                                                                                                                                                                                                                      NIM-1; noninducible immunity; systemic acquired resistance; SAR; pathogen; disease; protection; immunomodulated; plant; cereal; fruit; vegetable; virus; fungi; bacteria; insect; nematode; microbicide; ss.
                              1861 AICGTCGGTGAGACTCTTGCCTCTTAGTGTAATTTTTGCTGTACCATATAATTCTGT
                                                                                                 TTTCATGATGACTGTAACTGTTTATGTCTATCGTTGGCGTCATATAGTTTCGCTCTTCGT
                                                                                                            ATTCGACTTCTTCCACATCGAAATCAACCGGTGGAAAGAGGTCTAACCGTAAACTCTCTC
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/product= NIM-1
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96US-0034378
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resistance, such that the plants have a third level of resistance greater than the sum of the first two levels. The method can be applied to a wide variety of plants (cereals, fruits, oilseeds, vegetables etc.) to protect against viruses, fungi, bacteria, insects and nematodes. The method provides a high level of resistance and allows a reduction in the amount of micobloide used. Since the process involves two different methods of protection, it is unlikely that the pathogen will develop resistance to the treatment.
                                                                                                                                                            GATCTCTTTAATTTGTGAATTTCAATTCATCGGAACCTGTTGATGGACACCACCATTGAT 110
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ive 0; Mismatches
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Matches 2010; Conserv
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                                         ATGATCGCAAAACAAGCCACTATGGCGGTTGAATGTAATAATATCCCGGAGCAATGCAAG 1250
                                                                                                                                       ATTCCTAGAGATGTTCCTCCTCTTTTGCAGTGGCGGCCGATGAATTGAAGATGACGCTG 1370
                                                                                                                                                                                                                   CTCGATCTTGAAAATAGAGTTGCACTTGCTCAACGTCTTTTTCCAACGGAAGCACAAGCT 1430
GTCTCGAATGTACATAAGGCACTTGACTCGGATGATATTGAGTTAGTCAAGTTGCTTTTG 900
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             GCAATGGAGATCGCCGAAATGAAGGGAACATGTGAGTTCATAGTGACTAGCCTCGAGCCT
                                                                       CCGAGGGGATATACGGTGCTTCATGTTGCTGCGATGCGGAAGGAGCCACAATTGATACTA
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This sequence encodes a variant NIM-1 protein from Arabidopsis thaliana. This protein is used in a method resulting in the protection of an immunomodulated plant having a first level of resistance and involves treatment with at least 1 microbicide that confers a second level of resistance, such that the plants have a third level of resistance greater than the sum of the first two levels. The method can be applied to a wide variety of plants (cereals, fruits, oilseeds, vegetables etc.) to protect against viruses, fungi, bacteria, insects and nematodes. The method of micobicide used. Since the process involves two different methods of micobicide used. Since the process involves two different methods of protection, it is unlikely that the pathogen will develop resistance to
                                                                                                                                                                               NIM-1; noninducible immunity; systemic acquired resistance; SAR; pathogen; disease; protection; immunomodulated; plant; cereal; fruit; vegetable; virus; fungi; bacteria; insect; nematode; microblcide; ss.
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/note= "wild type TCC
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/note= "wild type TCG
2031 ACAATTTGAACCAATGGTATACAGATTTGTA
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Pred.
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                                                                                                                                                          thaliana NIM-1 cDNA variant #1.
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/product= NIM-1
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205..207
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Synthetic.
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P-PSDB; AAW64436.
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OY 1131 TCTCTATTGGAAAAAGGTGCAAGTGCATCAGAAGCAACTTTGGAAGGTAGAACCGCACTC 1190  OY 1131 TCTCTATTGGAAAAAGGTGCAAGTGCATCAGAAGCAACTTTGGAAGGTAGAACCGCACTC 1140  OV 1191 ATGATCGCAAAACAAGCCACTATGGAATGAAATATCCCGGAGGAATGCAAG 1250	1141 ATGATCGCAAAACAAGCCACTATGGCGGTTGAATGATAATAATATCCCGGAGCAATGCAAG	1231 CATTCTCTCAAAGGCCGACTATGTGTGTAAATACTAGAGCAAGAAGAAAAAGAAAAAGAAAAAAAA	1311 ATTCTRGAGATGTTCTCCCCTCTTTGCAGTGGCGGCCGATGAATGA		Qy 1431 GCAATGGGGAAATGGAGGAACATGTGAGTTCATAGTGACTAGCCTCGAGCCT 1490	Qy 1491 GACCGTCTCACTGGTACGAACGACATCACCGGGTGTAAAGATAGCACCTTTCAGAATC 1550	OY 1551 CTAGAAGAGCATCAAAGTAGACTAAAAGGGCTTTCTAAAACCGTGGAACTCGGGAAACGA 1610		Qy 1671 CTGGCTTGCGGAGAAGACACTGCTGAGAAACGACTACAAAAGAAGGAAAGGTACATG 1730  1021 CTGCCTTGCGGAGAAGACACTGCTGAGAAACGACTACAAAAGAAGGAAG			1 AAACTCTCTCATCGTCGGTGGGGTGAGACTCTTGCCTCTTAGTGTAATTTTGCTGTACCAT 191 	QY 1911 ATAATTCTGTTTTCATGATGACTGTAACTGTTTATGTCTATGGTTGGCGTCATAAGTTT 1970	1 CGCTCTTCGTTTTGCATCCTGTGTATTATTGC 	Oy 2031 ACANTTGAACCANTGGTATACACATTTGTA 2061	RESULT 4 AAV43661 ID AAV43661 standard; cDNA; 2011 BP.	AA AA AAV43661; XX XX 29-SEP-1998 (first entry)
Matches 2008; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  Qy 51 GATCTCTTTAATTTGTGAATTTCATCGGAACCTGTTGATGGACACCACCATTGAT 110	Qy         111         GGATTCGCCGATTCTTATGAAATCAGCAGCACTAGTTTCGTCGCTACCGATAACACCCAC         170           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	OY 171 TCCTCTATTGTTTATCTGCCGCGAACAAGTACTCACCGGACCTGATGTATCTGCTCTG 230	QY 231 CAATIGCTCTCCAACAGCTTCGAATCCGTCTTTGACTCGCCGGATGATTTCTACAGCGAC 290	291 GCTAAGCTTGTTCTCCGACGGCCGGGAAGTTTCTTTCCACCGGTGCGTTTTGTCAGCG 	351 AGAAGCTCTTTCTCAAGAGGGCTTTAGCCGCCGTAAGAAGAGAAAGACTCCAACAAC 1111111111111111111111111111	411 ACCGCCGCGCGGAAGCTCGAGGTTAAGGAGATTGCCAAGGATTACGAAGTCGGTTTCGAT	471 TCGGTTGTGACTGTTTTGGCTTATGTTTACAGCAGCAGCAGCAGCAGCCGCCCTAAAGGA 471 TCGGTTGTGACTGTTTTGGCTTATGTTTACAGCAGCAGCAGCAGCCGCCCTAAAGGA 471 TCGGTTGTGACTGTTTTTTTTTTACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGAAAGAA	421 ICGGIIGIONCIGIIIIGGCIIAIGII NCAGCAGCAGCAGCGCGCCGCCIGAGGGA 48 531 GTTTCTGAANGCGCAGACAGAATTGCTGCCCAGCGTGCCTTGCCGCCGGCGGTGGATTTC 59 111111111111111111111111111111111111	591 AIGTIGGAGGTTCTCTATTTGGCTTTCATCTTCAAGATCCCTGAATTAATT	651 CAGAGCCACTTATTGGACGTTGTAGACAAAGTTGTTATAGAGGACACATTGGTTATACTC 1111111111111111111111111111111	711 AAGCTTGCTAATATATGTGGTAAAGCTTGTATGAAGCTATTGGATAGATGTAAAGAGTTTTATTATTATGATAAAGAGTTTTTATTA	771 ATTGTCAAGTCTAATGTAGGTTAGGTTAGTCTTGAAAAGTCATTGCCGGAAGACCTTGTT 		891 GTCTCGAAFGTACATAAGGCACTTGACTCGGAFGATATTGAGTTAGTCAAGTTGCTTTTG 95 111111111111111111111111111111111111	Qy 951 AAAGAGGATCACCAATCTAGATGCGTGTGCTCTTCATTTCGCTGTTGCATATTGC 1010 	OY 1011 AATGTGAAGACGGCAACAGATCTTTAAAACTTGATCTTGCCGATGTCAACCATAGGAAT 1070 	OY 1071 CCGAGGGAFFAFGGTGCTTCAFGTTGCTGCGAAGGAGCCACAATTGATACTA 1130 1021 CCGAGGGGAFATACGGTGCTTCATGTTGCTGCGAAGGAGCCACAATTGATACTA 1080 DD 1021 CCGAGGGGAFATACGGTGCTTCATGTTGCTGCGGAAGGAGCCACAATTGATACTA 1080

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This cDNA encodes an altered form of the Arabidopsis thaliana non-
inducible immunity-1 (NIM1) protein. Sequences shown in AAV43661 to
AAV43665 represent variants of the NIM1 cDNA. The invention provides a
chimeric gene comprising a promoter active in plants operatively linked
co a DNA molecule that encodes an altered form of the NIM1 protein. Plant
cells stably transformed with a recombinant vector comprising such a
chimeric gene have a broad spectrum of disease resistance. The altered
conting transformed with a necombinant vector comprising such a
conting transformed with an altered NIM1 gene exhibits constitutive SAR
caquired resistance (SAR) signal transduction pathway. The transgenic
conformed with an altered NIM1 gene exhibits constitutive SAR
capterssion which is higher in the transformed plants than in a wild type
plant. The products can be used for producing plants with a broad
compounds that induce constitutive immunity (CIM) phenotype
cof inducer compounds that induce constitutive immunity (CIM) phenotype
cof in plants. The inventions can be used with plants such as rice, wheat,
chicory, lettuce, cabbage, cauliflower, broccoli, turnip, radish,
chicory, paparagus, onion, garlic, eggplant, pepper, celery, carrot,
squash, pumpkin, zucchini, cucumber, appie, pear, quince, mango, banana, soybean, tobacco,
cherry, peach, nectarine, apricot, strawberry, grape, raspberry,
charto, sorghum and sugarcane. The plants produced are resistant to
charty, sarphum and sugarcane. The plants produced can be used
in agriculture.
                                           Non-inducible immunity-1 gene; NIM1 gene; disease resistance; mutant; transgenic plant; SAR; systemic acquired resistance; CIM; pathogen; constitutive immunity; agriculture; variant; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Use of non-inducible immunity-1 gene - for transforming plants to produce transgenic plants having a broad spectrum disease resistance
              Non-inducible immunity-1 (NIM1) protein variant 1 encoding cDNA
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/note= "wild type TCG is replaced by GCG"
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/note= "wild type TGC is replaced by
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Synthetic.
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                                                                                                        GCTAAGCTTGTTCTCTCCGACGGCCGGGAAGTTTCTTTCCACCGGTGCGTTTTGTCAGCG
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   Seguence 2011 BP; 563 A; 417 C; 474 G; 557 T; 0 other;
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                       Score 2006.2;
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Matches 2008; Conservative
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Db	961	AATGTGAAGACCGCAACAGATCTTTTAAAACTTGATCTTGCCGATGTCAACCATAGGAAT 1020	ΩI	AAC377
δy	1071	CCGAGGGGATATACGGTGCTTCATGTTGCTGCGATGCGGAGGGGCCACAATTGATACTA 1130	¥ X	AAC377
QQ	1021	CCGAGGGGATATACGGTGCTTCATGTTGCTGCGATGCGGAAGGAGCCACAATTGATACT	XX	17-0CT
Οy	1131	TCTCTATTGGAAAAGGTGCAACTGCATCAGAAGCAACTTTGGAAGGTAGAACCGCACTC 1190	DE	Arabid
QQ	1081		KW K	Hybrid
ΟY	1191	ATGATCGCAAAACAAGCCACTATGGCGGTTGAATGTAATATTCCCGGAGCAATGCAAG 1250	X X X	protel
qq	1141		SO AA	Arabid
οy 1	1251	CATTCTCTCAAAGGCCGACTATGTGTAGAAATACTAGAGCAAGAAGACAAGAACAAAAAAAA	N X X	EP1033
op O	1201		PD	06-SEP
ογ	1311	ATTCCTAGAGATGTTCCTCCTCTTTTGCAGTGGCGCCCATGAATTGAAGATGAGCTG 1370	PF	25-FEB
QQ	1261	ATTCCTAGAGATGTTCCTCCTCTTTTGCAGTGGCGGCCGATGAATTGAAGATGACGCT	PR	25-FEB
Οy	1371	CICGAICTIGAAAATAGAGTIGCACTIGCICAACGICTITITICCAACGGAAGCACGAAAGCI 1430	- R R G	09 - MAR
QQ	1321		ች ዊ	25-MAR
οy	1431	GCAATGGAGATCGCCGAAATGAAGGGAACATGTGAGTTCATAGTGACTAGCCTCGAGCCT 1490	PR PR	29-MAR 01-APR
g	1381		PR PR	06-APR 08-APR
ογ	1491	15.5	PR	16-APR
. <u>q</u>	1441	) (	PR	21-APR
		4	A A A	23-APR 23-APR
Š 1	1551	CIAGAAGAGCATCAAAGTAGACTAAAAGGGCTTTCTAAAACCGTGGAACTCGGGGAAACGA 1610	PR	28-APR 30-APR
g G	1501		P.R.	30-APR
οž	1611	TTCTTCCGCGCGCTGTTCGGCAGTGCTCGACCAGATTATGAACTGTGAGGACTTGACTCAA 1670	. A. C	05-MAY
g	1561	TTCTTCCCCCGCTGTTCGGCTGCTCGACCAGATTATGAACTGTGAGGACTTGACTCAA 1620	P P	06-MAY
ρy	1671	CTGGCTTGCGGAGAAGACGACACTGCTGAGAACGACTACAAAAGAAGCAAAGGTACATG 1730	P. P.	07 - MAY 11 - MAY
QQ	1621		P. P.	14 - MAY
		C. C.C. 1. C.C. C.	P. P. R.	14 - MAY
δy	1731	GAAATACAAGAGACACTAAAGAAGGCCTTTAGTGAGGACAATTTGGAATTAGGAAATTCG 1790	PR	14 - MAY
qq	1681	GAAATACAAGAGACACTAAAGAAGGCCTTTAGTGAGGACAATTTGGAATTTGGAAATTTG 1740	PR	19-MAY
οy	1791	TCCCTGACAGATTCGACTTCTTCCACATCGAAATCAACCGGTGGAAAGAGGTCTAACCGT 1850	PR PR	20-MAY 21-MAY
qq	1741		PR	24 - MAY
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Q O	1801	AAACTCTCTCTCGTCGGTGAGACTCTTGCCTCTTAGTGTAATTTTTGCTGTACCAT 1860	PR	03-JUN
λά	1911	ATAATICIGITITCAIGAIGACIGITAACIGITTAIGICIATCGIIGGCGICATAIAGIIT 1970	A A	04 - JUN 07 - JUN
qq	1861	ATAATTCTGTTTTCATGATGACTGTAACTGTTTATGTCTATCGTTGGCGTCATATAGTTT 1920	PR PR	10-JUN
χ̈	1971	2.0	PR	10-JUN
g			PR	16-JUN
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9	1881	ACAATTTGAACCAATGGTATACAGATTTGTA 2011	PR PR	18-JUN 18-JUN
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RESULT 5

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ACA7765 standard; DNA; 2024 BP.

ACA7765;

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Arabidopsis thallana DNA fragment SEQ ID NO: 18587.

Arabidopsis thallana.

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                  GTGAAGCTCGAGCTTAAGGAGATTGCCAAGGATTACGAAGTCGGTTTCGATTCGGTTGTG
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ACTGGTACGAAGAGAACATCACCGGGTGTAAAGATAGCACCTTTCAGAATCCTAGAAGAG
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                        CCAACAGCTTCGAATCCGTCTTTGACTCGCCGGATGATTTCTACAGCGACGCTAAGCTTG
                                                                                TCTTCAAGAGCGCTTTAGCCGCCGCTAAGAAGGAGAAAGACTCCAACAACACCGCCGCCG
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Best Local Similarity 87.5%; Pred. No. 0;
Matches 2088; Conservative 0; Mismatche
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                              CGAGAACAAATTCCTAGAGATGTTCCTCCTCTTTTGCAGTGGCGGCCGATGAATTGAAG
                                                                                                         4195 AATTAAATTTATGTCCTCTCTATTAGGAAACTGAGTGAACTAATGATAACTATTGT
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Non-inducible immunity-1 gene; NIM1 gene; disease resistance; mutant; transgenic plant; SAR; systemic acquired resistance; CIM; pathogen; constitutive immunity; agriculture; ss.
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    A. thaliana non-inducible immunity-1 (NIM1) protein encoding DNA.

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4780..4782
/note= "this is indicated as TGG in a different
part of the specification"
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/product= "wild-type NIM1
/note= "contains introns"
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                                                                                                                       Location/Qualifiers
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       BP
       standard; DNA; 5655
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96US-0033177.
96US-0034379.
96US-0034382.
97US-0035021.
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Uknes SJ;
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27-DEC-1996;
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10-JAN-1997;
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vild-type protein. This DNA can be mutated to produce altered forms of the NIMM protein. This DNA can be mutated to produce altered forms of the NIMM protein. The invention provides a chimeric gene comprising a promoter active in plants operatively linked to a DNA molecule that cenceds an altered form of the NIMM protein. Plant cells stably transformed with a recombinant vector comprising such a chimeric gene have a broad spectrum of disease resistance. The altered NIMM proteins act as dominant-negative regulators of the systemic acquired resistance. CRAN's signal transduction pathway. The transgenic plants transformed with a natered NIMI gene exhibits constitutive SAR expression which is higher in the transformed plants with a broad spectrum disease resistance. Overexpression of NIMI minics the effects of inducer compounds that induce constitutive immunity (CIM) phenotype in plants. The inventions can be used with plants such as rice, wheat, barley, rye, corn, potato, carrot, sweet potato, sugar beet, bean, pea, chicory, lettuce, cabbage, cauliflower, broccoli, turnip, radish, spinach, asparagus, onion, garlic, eppple, pear, quince, melon, plum, cherry, peach, nectarine, apricot, strawberry, grape, raspberry, blackberry, pineapple, avocado, papaya, mango, banana, soybean, tobacco, tomato, sorghum and sugarcane. The plants produced are resistant to plant pathogens such as viruses, viroids, fungi, bacteria, insects such as aphids and lepidoptera and nematodes. The plants produced can be used in agriculture. the Arabidopsis thaliana non-inducible immunity-1 (NIM1) ×555555555555555555555555555555555

Sequence 5655 BP; 1758 A; 1014 C; 1069 G; 1814 T; 0 other;

3; 3054 TGAAGCTCGAGCTTAAGGAGATTGCCAAGGATTACGAAGTCGGTTTCGATTCGGTTGTGA 3174 CIGITITGGCTTATGTTTACAGCAGAGAGTGAGACCGCCGCCTAAAGGAGTTTCTGAAT 3234 540 649 240 TCTTCAAGAGCGCTTTAGCCGCCGCTAAGAAGGAGAAAGACTCCAACAACACCGCCGCCG 420 GCGCAGACGAGAATIGCIGCCACGIGGCTIGCCGGCGGCGGCGGIGGAITICAIGIIGGAGG 600 CCAACAGCTTCGAATCCGTCTTTGACTCGCCGGATGATTTCTACAGCGACGCTAAGCTTG 300 ATTIGIGAATTICAATICATCGGAACCIGITGATGGACACCACCATIGATGGATTCGCCG 120 1 TCGATCTTTAACCAAATCCAGTTGATAAGGTCTCTTCGTTGATTAGCAGAGATCTCTTTA 60 Gaps TGAAGCTCGAGCTTAAGGAGATTGCCAAGGATTACGAAGTCGGTTTCGATTCGGTTGTGA CTGTTTTGGCTTATGTTTACAGCAGAGTGAGACCGCCGCCCTAAAGGAGTTTCTGAAT TTTATCTGGCCGCCGAACAAGTACTCACCGGACCTGATGTATCTGCTCTGCAATTGCTCT TICICICGACGGCCGGGAAGITICITICCACCGGTGCGTTTTGTCAGCGAGAAGCTCTT Indels 298; Length 5655; 601 ITCICIATITGGCTTTCATCTTCAAGATCCCTGAATTAATTACTCTCTA---0; DB 19; Score 1760; DB Pred. No. 0; Mismatches 83.78; 87.58; Best Local Similarity 87.5 Matches 2088; Conservative Query Match 2995 3055 3175 3235 2755 3115 61 181 241 301 361 421 481 541 a g ò g ò g ò qq οy q ò g ò q ò q å q õ ò

q	95		354
Qy		9	4 9
QO	2	JATCTGCATTAAGCTATGGTTACACATTCATGAATATGTTCTTACTTGAGTACTTGTA 3	414
Qy	0	CAGAGGCACTTATTGGACGTTGTAGACAAAGTTGTTATAGAGGACACATTG 7	0.1
q	15	tgtatttcagaggcacttattggacgttgtagacaaagttgttatagagacacattg 3	474
Qy	702	TATACTCAAGCTTGCTAATATATGTGGTAAAGCTTGTATGAAGCTATTGGATAGAGT 7	61
qq	75	ATACTCAAGCTTGCTAATATATGTGGTAAAGCTTGTATGAAGCTATTGGATAGTGT 3	534
Qy	762	AAGTCTAATGTAGATATGGTTAGTCTTGAAAAGTCATTGCCGGAA 8	21
qq	32	SAGATTATTGTCAAGTCTAATGTAGATATGGTTAGTCTTGAAAAGTCTTTGCCGGAA S	, d
Qy	822	AATTGATAGACGTAAAGACCTTGGTTTGGAGGTACCTAAAGTA B	8 7
qq		<pre>SCTTGTTAAAGAGATAATTGATAGACGTAAAGAGCTTGGTTTGGAGGTACCTAAAGTA 3</pre>	1654
Ολ	882	ATGICTCGAATGTACATAAGGCACTTGACTCGGATGATATTGAGTTAACTCAAG SATGILLIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	4 1
q	3655	GAAACATGTCTCGAATGTACATAAGGCACTTGACTCGGATGATATTGAGTTAGTCAAG	1 T 4
03v	942	TGAAAGAGGATCACACCAATCTAGATGATGCGTGTGCTCTTCATTTCGCTGTT 1	1001
QQ Q	T	TGCTTTTGAAAGAAGGATCACAACCAATCTAGATGAATGA	
οy	02	IGCAATGTGAAGACCGCAACAGATCTTTTAAAACTTGATCTTGCCGATGTCAAC 1	5 :
ΟĎ	2	CATATTGCAATGTGAAGACCGCAACAGATCTTTAAAAACTTGATCTTGCCGATGTCAAC 🤅	æ
οy	90	APARTCCGAGGGGATATACGGTGCTTCATGTTGCTGCGATGCGGAAGGAGCCACAA 1	1121
QQ	3835	ataggaatccgagggatatacggtgcttcatgttgctgcgatgcggaaggagccacaa	68
δy	123	CAAGTGCATCAGAAGCAACTTTGGAAGGTAGA	18
qq	3895	CAAGTGCATCAGAAGCAACTTTGGAAGGTAGA	95
δλ	1182	CTATGGGGGTTGAATGTAATATATCCCGGAG	24
QQ	6	GGCACTCATGATCGCAAAACAAGCCACTATGGCGGTTGAATGTAATAATATCCCGGAG	0
QΥ	1242	TATGTGTAGAAATACTAGAGCAAGAAGACAAA	m
qq	$\vdash$	IGCAAGCATTCTCTCAAAGGCCGACTATGTGTAGAAATACTAGAGCAAGAAGACAAA	0
Qy		CCTCTTTTGCAGTGGCGCCGATGAATTGAAG	m
qq	4075	CCTCTTTTGCAGTGGCGCCCGATGAATTGAAG	
QY	1362	ATGACGCTGCTCGATCTTGAAAATAG	<u></u>
qq	4135	GTAICTAICAAGICTIAITICTIAIAIGITIG	Ξ.
Qy	1388		138
qq	4195	AACTGAGTGAACTAATGATAACTATTCTTTGT .	125
Qγ		AACGTCTTTTCCAACGGAAGCACAAGCTGCA	143
ò	4255	AACGICTITITCCAACGGAAGCACAAGCIGCA	4314
Qy	1434	GTGAGTTCATAGTGACTAGCCTCGAGCCTGAC	149
QQ	4315	GTGAGTTCATAGTGACTAGCCTCGAGCCTGAC	37.
Οy	1494	CCGGGTGTAAAGATAGCACCTTTCAGAATCCTA	1553

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                                                                                                  GAAGACGACACTGCTGAGAAACGACTACAAAAGAAGCAAAGGTACATGGAAATACAAGAG 1742
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                                                      1623 IGTTCGGCAGTGCTCGACCAGATTATGAACTGTGAGGACTTGACTCAACTGGCTTGCGGA
                                                                                  4495 CATCGGACTCCTTATCACAAAAACAAAACTAAATGATCTTTAAACATGGTTTTGTTACT
                                                                                                                                              TCGACTTCTTCCACATCGAAATCAACCGGTGGAAAGAGGTCTAACCGTAAACTCTCTCAT
                                                                                                                                                                           2043 AATGGTATACAGATTTGTAATATATTTTATGTACATCAACAATAA 2088
                                                                                                                                                                                                                                            noninducible immunity; disease resistance; plants;
           GAAGAGCATCAAAGTAGACTAAAAGCGCTTTCTAAAACC-
                                                                                                                                                                                                                                                                                                                                                                      protein"
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2787..3347
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                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana NIM1 gene.
                                                                                                                                                                                                                                                                             AAV04632 standard; DNA; 5655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence is that of the NIMI (noninducible immunity) gene. It may be used to confer a broad spectrum disease resistance in plants, specifically crop plants, e.g. rice, wheat, barley, rye and corn. The NIMI gene can be used to confer universal disease susceptibility to plant cells, and their progeny. It can also be used in a screening method for identifying compounds capable of inducing broad spectrum disease resistance in plants, while the plant cells, and their progeny, can be used to isolate a gene fragment which allows expression of broad spectrum disease resistance in plants, or to incorporate the resistant trait into plant lines through breeding.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIM1 gene which allows activation in plant of systemic acquired resistance - useful to confer broad spectrum disease resistance in plants, specifically crop plants, e.g. rice, wheat, barley, rye and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2695 TCGATCTTTAACCAAATCCAGTTGATAAGGTCTCTTGTTGATTAGCAGAGATCTTTA
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Weymann K;
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96US-0020272.
96US-0024883.
96US-0033177.
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13-DEC-1996;
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qq	4135		94
QΫ	1388	138	87
QQ	4195	AAATTTATGTCCTCTCTATTAGGAAACTGAGTGAACTAATGATAACTATTCTTTGT 42	54
0y	1388	TGCACTTGCTCAACGTCTTTTTCCAACGGAAGCACAAACTGCA 14	
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Qγ	1494	STCTCACTGGTACGAAGAGAACATCACCGGGTGTAAAGATAGCACCTTTCAGAATCCTA 15	2
QQ	4375	GAATCCTA 44	34
δy	1554	ATCAAAGTAGACTAAAAGCGCTTTCTAAAACC	92
QQ	4435	CATCAAAGTAGACTAAAAGCGCTTTCTAAAACGGGTATGGATTCTCACCCACTT 44	6
Qγ	1593	15	92
qq	4495	TCGGACTCCTTATCACAAAAACAAAACTAAATGATCTTTAAACATGGTTTTGTTACT 45	24
Qy	1593	Trcccccc 16	22
QQ	4555	sgaacregegaaacgarrerreeegee 46	
QY	1623	TGTTCGGCAGTGCTCGACCAGATTATGAACTGTGAGGACTTGACTCAACTGGCTTGCGA 168	182
QQ	4615	GTTCGGCAGTGCTCGACCAGATTATGAACTGTGAGGACTTGACTCAACTGGCTTGCGGA 46	274
δŏ.	89	GAAGACGACACTGCTGAGAAACGACTACAAAAGAAGCAAAGGTACATGGAAATACAAGA 174	42
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οp	4795	CGACTICTICCACATCGAAAICAACGGTGGAAAGAGGTCTAACCGTAAACTCTCTCAT 48	ń
δy	1863	6	2
qq	4855	GTCGTCGGTGAGACTCTTGCCTCTTAGTGTAATTTTTGCTGTACCATATAATTCTGTTT 49	-
Qy	1923	6	8
Dp	4915	CATGATGACTGTAACTGTTTATGTCTATGGGGGTCATATAGTTTGGCTCTTCGTTT 49	_
QY	1983	Ó	4
qq	4975	GCATCCTGTGTATTATTGCTGCAGGTGTGCTTCAAACAATGTTGTAACAATTTGAACC 50	34
δy	2043	TAATATATATTATGTACATCAACAAAA 208	
qq	5035	SGTATACAGATTTGTAATATATATTTATGTACATC	
RESU AAV4 ID	JLT 9 13658/C AAV43	658 standard; DI	
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ATTCTTATGAAATCAGCAGCACTAGTTTCGTCGCTACCGATAACACCGACTCCTCTATTG

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Non-inducible immunity-1 gene; NIM1 gene; disease resistance; mutant; transgenic plant; SAR; systemic acquired resistance; CIM; pathogen; constitutive immunity; agriculture; ss.
                                                                                                                                                                                                                                    Use of non-inducible immunity-1 gene - for transforming plants to produce transgenic plants having a broad spectrum disease resistance
thaliana non-inducible immunity-1 (NIM1) genomic sequence
                                                                                                                                                                                              HY;
                                                                                                                                                                                              Steiner
                                                                                                                                                                                             Ryals JA,
                                                                                                                                                                                                                                                         Example 11; Pages 98-107; 205pp; English.
                                                                                                                                                                                                                                  non-inducible immunity-1 gene
                                                                                                                                                                                             KA,
                                                                                                                                                                                             Lawton
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96US-0033177.
96US-0034382.
97US-0034730.
97US-0035021.
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                                              Arabidopsis thaliana
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                                                                                                                                                                             (NOVS ) NOVARTIS AG
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This represents the genomic sequence of the Arabidopsis thaliana noninducible immunity-1 (NIM1) gene. The invention provides a chimeric gene comprising a promoter active in plants operatively linked to a DNA molecule that encodes an altered form of the NIM1 protein. Plant cells stably transformed with a recombinant vector comprising such a chimeric gene have a broad spectrum of disease resistance. The altered NIM1 CC can stance (SAR) signal transduction pathway. The transgenic plants proteins act as dominant-negative regulators of the systemic acquired resistance (SAR) signal transduction pathway. The transgenic plants constitutive SAR campromed with an altered NIM1 gene exhibits constitutive SAR capprocraces and altered NIM1 gene exhibits constitutive SAR capprocraces are seistance. Overexpression of NIM1 mimics the effects of inducer compounds that induce constitutive immunics the effects of inducer compounds that induce constitutive immunics the effects of inducer compounds that induce constitutive immunics the effects of inducer compounds that induce constitutive immunics the effects of inducer compounds that induce constitutive immunics the effects of inducer compounds that induce constitutive immunics the effects of inducer compounds that induce constitutive immunic, clm, peach, peach nematodes. The plants produced can be used pathogens such as viruses, aphids and lepidoptera and agriculture.

Sequence 9919 BP; 3150 A; 1825 C; 1737 G; 3207 T; 0 other;

DB 19; Length 9919;

3 Gaps Indels 298; 0; Score 1760; DB Pred. No. 0; 0; Mismatches Query Match 83.7%; Best Local Similarity 87.5%; Matches 2088; Conservative ð

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3448 3148 3147 TTTGTATTTCAGAGGCACTTATTGGACGTTGTAGAGAAGTTGTTATAGAGGACACATTG 3088 TTGCTTTTGAAAGAGGATCACACCAATCTAGATGATGCGTGTGCTCTTCATTTCGCTGTT 1001 1122 TTGATACTATCTCTATTGGAAAAGGTGCAAGTGCATCAGAAGCAACTTTGGAAGGTAGA 1181 761 821 941 3207 ACCATCTGCATTAAGCTATGGTTACACATTCATGAATATGTTCTTACTTGAGTACTTGTA TTTATCTGGCCGCCGAACAAGTACTCACCGGACCTGATGTATCTGCTCTGCAATTGCTCT CCAACAGCTTCGAATCCGTCTTTGACTCGCCGGATGATTTCTACAGCGACGCTAAGCTTG TTCTCTCCGACGCCGGGAAGTTTCTTTCCACCGGTGCGTTTTGTCAGCGAGAAGCTCTT TGAAGCTCGAGCTTAAGGAGATTGCCAAGGATTACGAAGTCGGTTTCGATTCGGTTGTGA GAGCTTGTTAAAGAGATAATTGATAGACGTAAAGAGCTTGGTTTGGAGGTACCTAAAGTA TCTTCAAGAGGGCTTTAGCCGCCGCTAAGAAGGAGAAAGACTCCAACAACACCGCCGCCG CTGTTTTGGCTTATGTTTACAGCAGAGTGAGACCGCCGCCCTAAAGGAGTTTCTGAAT -----TCAGAGGCACTTATTGGACGTTGTAGACAAAGTTGTTATAGAGGACACATTG AAAGAGATTATTGTCAAGTCTAATGTAGATATGGTTAGTCTTGAAAAGTCATTGCCGGAA GTTATACTCAAGCTTGCTAATATATGTGTAAAGCTTGTATGAAGCTATTGGATAGATGT AAGAAACATGTCTCGAATGTACATAAGGCACTTGACTCGGATGATATTGAGTTAGTCAAG TTGCTTTTGAAAGAGGATCACACCAATCTAGATGCGTGTGTGCTCTTCATTTCGCTGTT GCATATTGCAATGTGAAGACCGCAACAGATCTTTTAAAACTTGATCTTGCCGATGTCAAC CATAGGAATCCGAGGGGATATACGGTGCTTCATGTTGCTGCGATGCGGAAGGAGCACAA 3567 3747 3687 3627 3507 3447 3327 3267 3087 2967 2907 2847 1002 2787 181 301 421 481 3387 541 601 650 702 762 3027 822 882 1062 241 361 650 942 g δλ g qq qq g qq QQ οp Q δ δ δy δλ δy qq δλ q g Q Ωp qq QQ ŏ QΫ́ Qγ δλ qq οy Qy Dp δλ qq ó QY Qγ

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                                  CGTCTCACTGGTACGAAGAGAACATCACCGGGTGTAAAAGATAGCACCTTTCAGAATCCTA
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The sequence is that of the 9.9kb region of clone BAC-04 containing the NIM1 (noninducible immunity) gene. It may be used to confer a broad spectrum disease resistance in plants, specifically crop plants, e.g. rice, wheat, barley, rye and corn. The NIM1 gene can be used to confer universal disease susceptibility to plant cells, and their progeny. It can also be used in a screening method for identifying compounds capable of inducing broad spectrum disease resistance in plants, while the plant cells, and their progeny, can be used to isolate a gene fragment which allows expression of broad spectrum disease resistance in plants, or to incorporate the resistant trait
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIM1 gene which allows activation in plant of systemic acquired resistance - useful to confer broad spectrum disease resistance in plants, specifically crop plants, e.g. rice, wheat, barley, rye and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TCGATCTTTAACCAAATCCAGTTGATAAGGTCTCTTCGTTGATTAGCAGAGATCTCTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 9919;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 9919 BP; 3150 A; 1826 C; 1737 G; 3206 T; 0 other;
                                                                                                                                                                                                                                                                                                                  NIM1; noninducible immunity; disease resistance; plants; SAR gene expression; ss.
                   AATGGTATACAGATTTGTAATATATTTATGTACATCAACAATAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                             the NIM1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Johnson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1760; DB
Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                             containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Friedrich | Weymann K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             into plant lines through breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 4; Fig 14; 153pp; English.
                                                                                                                                                 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Weymann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97US-0035022.
96US-0020272.
96US-0024883.
96US-0033177.
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llarity 87.5%;
Conservative (
                                                                                                                                                                                                                                                                          thaliana BAC-04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96US-0773559
                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ellis DM,
Ryals JA,
                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana
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                                                                                                                                               AAV04631 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 2088; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUN-1996;
30-AUG-1996;
13-DEC-1996;
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                                                                                                                                                                                                                                                                             Arabidopsis
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TG 18 	CT 24 		TT 36      35	CG 42	GA 48     GA 33	T 54  - T 33	ig 60 - ig 32	- 64 C 32	- 64	A 31	'G 701    G 308	GT 76      30	82	4 88 4 29	3 94	10 27	2 10	11 26
CTAT       CTAT	TGCT 	AAGCTJ            AAGCTJ	3CTC	0900	rrer      rrer	TCTGAA:        TCTGAA:	TGGAG       TGGAG	TAAAA	:	CTTGT	ACATT	AGAT       AGAT	CCGGAA 	AAAGT/       AAAGT/	GTCAAC GTCAAC	GCTGTT        GCTGTT	GTCAAC        GTCAAC	CCACAA        CCACAA
CTCCT	GCAAT 	301	GAGAA(       GAGAA(	CACCG	TTCGG	311	ATGT	TCAGGT	-	GAGTA	AGGACAC         AGGACAC	GAT	ATTGC 	GTACCT.        GTACCT.	STTA      STTA	ATTTC         ATTTC	CGAT	3AG
ACCGA       ACCGA	CICI	CAGCGAC	CAGC CAGC	A = A	TCGA       CGA	TAAAGGA(          TAAAGGA(	GATTTC/        GATTTC/	CTA CTA	-	ACTT	ATAGAC         ATAGAC	GAAGCTATTG	IGAAAAGTCATTG 	GAG    GAG	ATTGAC        ATTGAC		CTTGC	CGGAAGO            CGGAAGO
ATAAC?	ATCTG       ATCTG	CIP	TTTGT       TTTGT	CTCCAA(        CTCCAA(	CGGTT	GCCTA	GGTGG       GGTGG	TACTCT(		PTCTT	TGTT	rgaag       rgaag		rrig 	ATGATATS 	GTGCT       GTGCT	TGAT	CGATG       CGATG
8 - 8	GATGT/        GATGT/	GATTT         GATTT	SCGT SCGT	<u> </u>	GAAGT	0000	0990	TAATT	!	TATGT	AAAG HIH AAAG	TGTATC	AGTCT:	CTTGG	CTCGG1	GCGT	FAAAACTTGATC 	6016 
CGCTAC	GACCTC	GGAT      GGAT	CCGGT(	GGAGAAAG          GGAGAAAG	TAC	GAGAC       GAGAC	25522 25522 25522	TGAAT:       TGAAT		ATGAAT	GTAGAC.	AAAGCTT	rggtt2        rggtt2	AAAGAGC	45 – 45	ATGAT       ATGAT	CTTTTA	CATGTT
TTCGT 	82	10000 1-1-1 10000	TTCCA(	AAGAAC IIIII AAGAAC	AAGGAT          AAGGAT	AGAGT	GCTTG       GCTTG	GATCCCT            GATCCCT		ATTCA	TE E	361	AGATATO          AGATATO	5 - 5	GCACTTC 	CTAGATGAT 	AGATC:	GCTTC2       GCTTC2
CTAGT	GTACTCA(	CTTTGACT               CTTTGACT	GTTTCTTTC	CCGCTAAC	S = S	CAGC	CGTG       -	8=8	1	GGTTACACAT	TGGACC        TGGACC	ATATGTC	AATGT# 	GATAGACC	TACATAAGGC	ACACCAATC	CAAC	ACGGTG             ACGGTG
CAGCAC          CAGCAC	¥=8	828	4 = 4 4 = 4 4 = 4	9008 	GAGATTG(         GAGATTG(	TTACAG         TTACAG	TGCCA	ATCTTC        ATCTTC	:	Ė	CTTAT	raat      raat	CAAGTCTA               CAAGTCTA	ATT	55 = 55	GATCACA 		턴트턴
SAG SAG	CCGAAC	GAATCC	95008 	CTTTA        CTTTA	CTTAAGC	ATGTT 	ATTGC 	CTTTCA	-	AAGCT	NGGCACT	CTTGC	GTCAA(        GTCAA(	GCTTGTTAAAGAGATA 	CGAATC	AGGAZ       AGGAZ	rgtgaagacce 	GAGGGGATA 
TGAAATC         TGAAATC	92299 	CTTCG	GACG      GACG	GAGCG(        GAGCG(	SAG SAG	SCT	GAGAAT	TTGG	:	CATT	-TCAGA(       TTCAGA(	CAAG        CAAG	ratt      ratt	TAAAG TAAAG	rgrer       rgrer	GAAAGAGG 	CAAT	TCCGA 
CTTA	ATCT       ATCT	AACAGO 	TCTCO  - - - TCTCO	rcaa ICAA	AGCTC(	TTTIG        TTTIG	CAGAC         CAGAC	TCTAT       TCTAT		ATCTG		ATACT        ATACT	GAGAT	TTGT	AAGAAACATG 	CTTTT        CTTTT	TATTG	AGGAATCCG 
1 ATT     7 ATT	1 TTT 1	1 CCA 	TTCT	1CT	TGAA(	CTG	929  929	TTC		ACC	TTT	GTT	AAA   AAA	GAC GAC		116	GCA GCA	CATA
121 3747	181	241	301 3567	361	421	3387	541	601 3267	650	3207	650 3147	702 3087	762 3027	822 2967	882 2907	942	1002 2787	1062 2727
Qy Dp	oy Db	Qy	Qy Db	Oy Dp	Qy	Qy Dp	Qy Dp	Qy Dp	δλ	QQ	QY Dp	Qy Db	Qy Db	Qy	Qy Db	QY Db	Oy Db	Oy Dp

1182   ACCGGARCTCATGATCGCAAAACACCACTATGGCGGTGCAATGATAATAATATGCCGGAA   2407   ACCGGARCTCATGGAAAACCACTATGGCGGTGCAATGAAATTCCCCGGAAAAACCCCGAAAAACCCCGAAAAAACCCCGAAAAACCCCGAAAAACCCCGAAAAACCCCGAAAAATTCCTCAAAGCCCCATTTTGCAGTGCGCGCGATGAATTCAAGAAAAACCCCGTTTTTGCAGTGCGCGCGTGCAAATTCAAGAAATTCCTCAAAAATTCCTCCACTCTCTTTTGCAGTGCGCGCGATGAATTCAAGAAAATTCCTCAAAAAA	QY	1122	TIGHTH	~ ~
1242 CAATGCAAGCATTCTC 2547 CAATGCAAGCATTCTC 1302 CGAGAACAATTCCTF 13102 CGAGAACAAATTCCTF 1312 ATGACGCTGCTCGATC 1318	გ ფ	18	ACCGCACTCATGATCGCAAAACAAGCCACTATGGCGGTTGAATGTAATATATCCC 	1241
1302 GGAGAACAAATTCCTR 1362 ATGAGCTGCTGATG 1362 ATGAGCTGCTGATG 1388	2y 3b	24	CAATGCAAGCATTCTCTCAAAGGCCGACTATGTGTAGAAATACTAGAGGAAGAGCA 	130
1362 ATCACGCTCCATC 1362 ATCACGCTCCATC 1368	λ. 4	30:	CGAGAACAAATTCCT	36
2427 ATCACGCTCGATC  1388	9 &	36.	CGAGAACAAATTCCTF ATGACGCTGCTCGATC	42
1388	. q	42	ATGACGCTGCTCGATC	36
2367 AATTAAATTTATGTCC  1388	ζλ	38		38
1388	q	36,	AATTAAATTTATGTCC	30
1434 ATGGAGATCGCGAAA 1494 CGTCTCACTGGTACGA 1494 CGTCTCACTGGTACGA 1197 CGTCTCACTGGTACGA 1554 GAAGAGCATCAAAGTA 1559 AAGAGCATCAAAGTA 1593	. A	386	GTCGTCCACTGTTTAG	43
1494 CGTCTACTGGTACGAGAGAACATCACGG 1494 CGTCTACTGGTACGAGAGAACATCACCGG 2187 CGTCTACTGGTACGAGAGAACATCACCGG 1554 GAAGAGCATCAAAGAGACATCACCGG 1554 GAAGAGCATCAAAGTAGACTAAAAGCGCTTT 1593	λ .	43	GAAA	49
153 CGTCTCACTGCTAAAAAAACATCACGG 1554 GAAGAGCATCAAAGTAGAACATCACGGG 1554 GAAGAGCATCAAAGTAGACATCACGGG 1554 GAAGAGCATCAAAGTAGACATCACGGGTTT 2127 GAAGAGCATCAAAGTAGACTAAAAGCGCTTT 2127 GAAGAGCATCAAAGTAGACTAAAAGCGCTTT 1593	;	1 2		0 1
1554 GAAGAGCATCAAAGTAGACTAAAAGGGGTTT  2127 GAAGAGCATCAAAGTAGACTAAAAGCGCTTT  1593	Z - 2	18	GILILALIGGIALGAAGAGAACAICACGG 	155
2127 GAAGAGCATCAAAGTAGACTAAAAGCGGTTT  1593	λ	55	AAGAGCATCAAAGTAGACTAAAAAGCGCTTT	159
1593	ð	12	AAGAGCATCAAAGTAGACTAAAAGCGCTTT	506
2067 CATCGGACTCCTTATCACAAAAACAAAACT 1593	λ	59		159
1593	ą	90	atcggactccttatcacaaaaaacaaaact	500
2007 TGCTGTCTGACCTTGTTTTTTTTGTCATGGGGGGGGGGG	¥	59	9	162
1623 TGTTCGGCAGTGCTCGACCAGATTATGAACTGTGGGGACTTGACGCGTTGCGGGGGTTGCGCGGCAGTGCTCGCGACCAGACTTATGAACTGTGAGGACTTGACTGCGCACCAGCAGATTATGAACTGTGAGGACTTGACTGCGCGTTGCGGGGGGGG	ā	.00	GCTGTCTGACCTTGTTTTTTTTTTATCATCAGGAACTCGGGAAACGATTCTTCCCGCG	94
1683 GAAGACCACTGCTGACAACACACACACACACACTGCACATGCACATGCACATGCACATGCACACGGGGGGGG	<u>≯</u> 4	62	GTTCGGCAGTGCTCGACCAGATTATGAACTGTGAGGACTTGACTCAACTGGCTTGCG THILLIHIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	1682
1887 GAAGACGACTGCTGAGAAACGACTACAAAAGAAGGAAAGGTACATGGAAATGAAGGAAAAGGACTACAAAGGACTACAAAAGAAAG	>	99	SACGACACTGCTGAGAAACGACTACAAAAAGAAAGGAAAG	74
1743 ACACTAAAGAAGGCCTTTAGTGAGGACAATTTGGAATTAGGAAATTCGTCCCTGACAG	۾ ،	.88		. ~
1827 ACACTAAAGAGCCTTTAGIGITIIIIIIIIIIIIIIIIII	Δī	74	ACTAAAGAAGGCGTTTAGTGAGGACAATTTGGAATTAGGAAATTCGTCCTGACAG	0
1803 TCGACTTCTCCACATCGAAATCAACGGTGGAAAGAGGTCTAACCGTAAACTCTCT	ą	82.		76
1767 TCGACTTCTCCACATCGAATCAACGGGGGGAAGGGGTCTAACCGTAAACTCTTTTTTTT	×	80	CGACTTCTTCCACATCGAAATCAACCGGTGGAAAGAGGTCTAACCGTAAACTCTCT	9
1863 CGTCGTCGGTGAGACTCTTGCCTTAGTGTAATTTTGCTGTACCATATAATTCTGTT	Q	.97	CGACTTCTTCCACATGGAAATCAACGGGGGGGAAAGAGGGGTTAACCGTAAACTCTCT	70
1707 CGTCGTCGGTGAGTCTTTGCTTTTTTTTTTTTTTTTTTT	γ	96	STCGTCGGTGAGACTCTTGCCTCTTAGTGTAATTTTTGCTGTACCATATAATTCTGTT	2
1923 TCATGATGACTGTAACTGTTTATGTCTTGGCGCCCATATAGTTTCGCTCTTCGTT	q	70	GTCGTCGGTGAGACTCTTGCCTCTTAGTGTAATTTTTGCTGTACCATATAATTCTGT	64
1647 TCATGATGATGTAACTGTTTATGTCTATGGTTGGCGTCATATAGTTTCGCTCTTCGTT 1983 TGCATCCTGTATATTGCTGCAGGTGTGTTCAAACAATGTTGTAACAATTTGAAC	۸ .	92.	CATGATGACTGTAACTGTTTATGTCTATCGTTGGCGTCATATAGTTTCGCTCTTC	
1983 IGCATCCTGIGTATTATTGCTGCAGGTGTGCTTCAAACAAATGTTGTAACAATTTGAAC	q	64	CATGATGACTGTAACTGTTATGTCTATCGTTGGCGTCATATAGTTTCGCTCTTCGTT	1588
	5	98.	GCATCCTGTGTATTATTGCTGCAGGTGTGCTTCAAACAAA	2042

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                                                                                                                                                                  bacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TCGATCTTTAACCAAATCCAGTTGATAAGGTCTCTTCGTTGATTAGCAGAGATCTCTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTCTTATGAAATCAGCAGCACTAGTTTCGTCGCTACCGATAACACCGACTCCTTATTG
                                                                                                                                                                                                                                                                                                                                                                    New isolated plant acquired resistance polypeptide gene - useful for, e.g. producing plants with increased resistance to pathogens such as bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 19; Length 7548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   298;
                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence is that of a 7.5 kb genomic region which contains the acquired resistance gene NPRI. The gene may be used in the production of transgenic cells which can produce the encoded acquired resistance protein. Such transgenic plants cells are useful in the production of plants having an increased level of resistance against disease caused by plant pathogens, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seguence 7548 BP; 2347 A; 1468 C; 1397 G; 2336 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nematodes, viruses,
                                                                                                                                                                 gene; acquired resistance; disease; plant pathogens; plasma; fungi; insects; nematodes; viruses; viroids;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                    AATGGTATACAGATTTGTAATATATATTTTATGTACATCAACAATAA
                                                                                                                                               thaliana 7.5kb region containing NPR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83.1%; Score 1748.4;
87.5%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                         Glazebrook
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bacteria, mycoplasmas, fungi, insects,
                                                                                         ВР
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                                                                                         AAV16850 standard; DNA; 7548
                                                                                                                                                                                                                                                                           97US-0046769.
96US-0023851.
97US-0035166.
                                                                                                                                                                                                                                                          97WO-US13994
                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                          Dong
                                                                                                                                                                                                                                                                                                                HOSPITAL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 87.5
Matches 2087; Conservative
                                                                                                                                                                                                    Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-159458/14
                                                                                                                                                                                                                                                                                                                (GEHO ) GEN HOSPIT
(UYDU-) UNIV DUKE.
                                                                                                                                                                                   transgenic; ds.
                                                                                                                                                                                                                                                                            16-MAY-1997;
09-AUG-1996;
10-JAN-1997;
                                                                                                                                                                                                                       WO9806748-A1
                                                                                                                                                                                                                                                          38-AUG-1997;
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This sequence encodes a truncated variant NIM-1 protein from Arabidopsis thaliana. This protein is used in a method resulting in the protection of an immunomodulated plant having a first level of resistance and involves treatment with at least 1 microbicide that confers a second level of resistance, such that the plants have a third level of resistance greater than the sum of the first two levels. The method can be applied to a wide variety of plants (cereals, fruits, oilseeds, vegetables etc.) to protect provides a high level of resistance and allows a reduction in the amount of micobicide used. Since the process involves two different methods of protection, it is unlikely that the pathogen will develop resistance to
                                                                                                                                                                                                                                                                                                                                                                                                               NIM-1; noninducible immunity; systemic acquired resistance; SAR; pathogen; disease; protection; immunomodulated; plant; cereal; fruit; vegetable; virus; fungi; bacteria; insect; nematode; microbicide; ss.
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C-terminal truncated NIM-1 variant cDNA.
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100.0%; Pred. No. 0;
.ive 0; Mismatches 0;
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Matches 1605; Conservative
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                                                                                                                                 CATTCTCTCAAAGGCCGACTATGTGTAGAAATACTAGAGCAAGAAGAACAAACGAGAACAA
         wild-type
                                 ATTCCTAGAGATGTTCCTCCCTCTTTTGCAGTGGCGGCCGATGAATTGAAGATGACGCTG
                                                                  CTCGATCTTGAAAATAGAGTTGCACTTGCTCAACGTCTTTTTCCAACGGAAGCACAAGCT
                                                                                                   GCAATGGAGATCGCCGAAATGAAGGGAACATGTGAGTTCATAGTGACTAGCCTCGAGCCT
                                                                                                                                                                    CTAGAAGAGCATCAAAGTAGACTAAAAGCGCTTTCTAAAACCGTGGAACTCGGGAAACGA
                                                                                                                                                                                                                                                                                                               Non-inducible immunity-1 (NIM1) protein variant 3 encoding cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    НY;
                                                                                                                                                                                                                                                                                                                                                                                                               /product= "NIM1 protein variant 3"
/note= "C-terminal deletion compared to
NIM1 sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Steiner
                                                                                                                                                                                                      TTCTTCCCGCGCTGTTCGGCAGTGCTCGACCAGATTATGAACTGT
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                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                                                                                                              CDNA; 1608
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96US-0033177.
96US-0034379.
96US-0034382.
97US-0035021.
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                                                                                                                                                                                                                                                               AAV43663 standard;
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Uknes SJ;
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13-DEC-1996;
27-DEC-1996;
27-DEC-1996;
10-JAN-1997;
10-JAN-1997;
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AAV43663
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Use of non-inducible immunity-1 gene - for transforming plants to produce transgenic plants having a broad spectrum disease resistance

Claim 12; Pages 155-159; 205pp; English.

This cDNA encodes an altered form of the Arabidopsis thaliana noninducible immunity-1 (NIMI) protein. Sequences shown in AAV43661 to
AAV43665 represent variants of the NIMI cDNA. The invention provides a
chimeric gene comprising a promoter active in plants operatively linked
to a DNA molecule that encodes an altered form of the NIMI protein. Plant
cells stably transformed with a recombinant vector comprising such a
chimeric gene have a broad spectrum of disease resistance. The altered
chimeric gene have a broad spectrum of disease resistance. The altered
continued set as dominant-negative regulators of the systemic
continued resistance (SAR) signal transduction pathway. The transgenic
plants transformed with an altered NIMI gene exhibits constitutive SAR
expression which is higher in the transformed plants than in a wild-type
continued products can be used for producing plants with a broad
spectrum disease resistance. Overexpression of NIMI mimics the effects
of inducer compounds that induce constitutive immunity (CIM) phenotype
confidence compounds that induce constitutive immunity (CIM) phenotype
conforty, lettuce, cabbage, cauliflower, broccoli, turnip, radish,
conforty, lettuce, cabbage, cauliflower, broccoli, turnip, radish,
conforty, planty, pincapple, avcoado, papaya, mango, banana, soybean, tobacco,
conforty, planty, pincapple, avcoado, papaya, mango, banana, soybean, tobacco,
conforty, planty pathogens such as viroids, fundi, bacteria, insects such
conforty and lepidoptera and nematodes. The plants produced can be used
conforty in a pathogen be negative the plants produced can be used in agriculture.

Sequence 1608 BP; 447 A; 340 C; 385 G; 436 T; 0 other;

ó 410 230 240 300 470 420 590 51 GATCTCTTTAATTTGTGAATTTCAATTCATCGGAACCTGTTGATGGACACCACCATTGAT 110 121 TCCTCTATTGTTTATCTGGCCGCCGAACAAGTACTCACCGGACCTGATGTATCTGCTCTG 180 GCTAAGCTTGTTCTCTCCGACGCCCGGGAAGTTTCTTTCCACCGGTGCGTTTTGTCAGCG 350 AGAAGCTCTTTCTTCAAGAGCGCTTTAGCCGCCGCTAAGAAGGAGAAAAGACTCCAACAAC Gaps TCGGTTGTGACTGTTTTGGCTTATGTTTACAGCAGCAGAGGAGCCGCCGCCTAAAGGA 111 GGATTCGCCGATTCTTATGAAATCAGCAGCACTAGTTTCGTCGCTACCGATAACACCGAC TCCTCTATTGTTTATCTGGCCGCCGAACAAGTACTCACCGGACCTGATGTATCTGCTCTG 231 CAATTGCTCTCCAACAGCTTCGAATCCGTCTTTGACTCGCCGGATGATTTCTACAGCGAC AGAAGCTCTTTCTTCAAGAGCGCTTTAGCCGCCGCTAAGAAGGAGAAAGACTCCAACAAC ACCGCCGCCGTGAAGCTCGAGCTTAAGGAGATTGCCAAGGATTACGAAGTCGGTTTCGAT 0; Score 1605; DB 19; Length 1608; Pred. No. 0; Indels 0; Query Match 76.3%; Score 1605; D Best Local Similarity 100.0%; Pred. No. 0; Matches 1605; Conservative 0; Mismatches Query Match 181 171 291 351 301 411 361 471 121 531 g δλ a οχ g b Q δλ qq δλ q ò q οχ Q ò ò

1070 1020 1080 1250 1430 1010 950 900 096 770 720 830 780 890 710 099 AATGTGAAGACCGCAACAGATCTTTTAAAACTTGATCTTGCCGATGTCAACCATAGGAAT 1081 TCTCTATTGGAAAAAGGTGCAAGTGCATCAGAAGCAACTTTGGAAGGTAGAACCGCACTC ATGATCGCAAAACAAGCCACTATGGCGGTTGAATGTAATATATCCCGGAGCAATGCAAG CATTCTCTCAAAGGCCGACTATGTGTAGAAATACTAGAGCAAGAAGACAAACGAGAACAA ATTCCTAGAGATGTTCCTCCTCTTTTGCAGTGGCGGCCGATGAATTGAAGATGACGCTG ATTCCTAGAGATGTTCCTCCTCTTTTGCAGTGGCGGCCGATGAATTGAAGATGACGCTG CAGAGGCACTTATTGGACGTTGTAGACAAAGTTGTTATAGAGGACACATTGGTTATACTC **AAGCTTGCTAATATATGTGGTAAAGCTTGTATGAAGCTATTGGATAGATGAAAGAGATT** AAAGAGATAATTGATAGACGTAAAGAGCTTTGGTTTGGAGGTACCTAAAGTAAAGAAACAT GTCTCGAATGTACATAAGGCACTTGACTCGGATGATATTGAGTTAGTCAAGTTGCTTTTG AAAGAGGATCACACCAATCTAGATGATGCGTGTGCTCTTCATTTCGCTGTTGCATATTGC CCGAGGGGATATACGGTGCTTCATGTTGCTGCGATGCGGAAGGAGCCACAATTGATACTA TCTCTATTGGAAAAAGGTGCAAGTGCATCAGAAGCAACTTTGGAAGGTAGAACCGCACTC CTCGATCTTGAAAATAGAGTTGCACTTGCTCAACGTCTTTTTCCAACGGAAGCACAAGCT GCAATGGAGATCGCCGAAATGAAGGGAACATGTGAGTTCATAGTGACTAGCCTCGAGCCT GACCGTCTCACTGGTACGAAGAGAACATCACCGGGTGTAAAGATAGCACCTTTCAGAATC CTAGAAGAGCATCAAAGTAGACTAAAAGCGCTTTCTAAAACCGTGGAACTCGGGAAACGA ATTGTCAAGTCTAATGTAGATATGGTTAGTCTTGAAAAGTCATTGCCGGAAGAGCTTGTT TICITCCCCCCCCCTCTCCCCACTCCTCCACCACATTAICAACTGT 1655 1011 1261 1561 781 891 841 901 1071 1021 1131 1191 1141 1251 1201 1311 1371 1321 1431 1381 1491 1551 1501 1611 651 601 711 199 721 831 951 961 481 771 591 g g ρp g QY d οg q ŏ g ò q ŏ pp g Dp g g Pp ò g Qγ Ω ò QΥ δ à Q δ QY Qγ 9 QY Q

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             582
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                                                                                                                NIM-1; noninducible immunity; systemic acquired resistance; SAR; pathogen; disease; protection; immunomodulated; plant; cereal; fruit; vegetable; virus; fungi; bacteria; insect; nematode; microbicide; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Protection of immunomodulated plants against pathogens applying microbicide to provide increase in resistance
                                                                                             thaliana N-terminal truncated NIM-1 variant cDNA #1.
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Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 14; Page 123-127; 164pp; English.
                                                                                                                                                                                            Location/Qualifiers
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/*tag= a
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                              BP
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/note= "variant"
                              AAV46276 standard; cDNA; 1597
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Best Local Similarity 99.9%;
Matches 1594; Conservative
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                                                                        (first entry)
                                                                                                                                                               Arabidopsis thaliana.
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P-PSDB; W6447.
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                                                                                                    TTTTGAAAGAGGATCACAACCAATCTAGATGATGCGTGTGCTCTTCATTTCGCTGTTGCAT
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ATTCGTCCCTGACAGATTCGACTTCTTCCACATCGAAATCAACCGGTGGAAAGAGGTCTA 1845
                                                                       ACCGTAAACTCTCTCATCGTCGTCGTGAGACTCTTGCCTCTTAGTGTAATTTTTGCTGT 1905
ACATGGAAATACAAGAGACACTAAAAGAAGGCCTTTAGTGAGGACAATTTGGAATTAGGAA 1785
                                     Non-inducible immunity-1 gene, NIM1 gene, disease resistance; mutant; transgenic plant; SAR; systemic acquired resistance, CIM; pathogen; constitutive immunity; agriculture; variant; ss.
                                                                                                                                     ACCATATAATTCTGTTTTCATGATGACTGTAACTGTTTATGTCTATCGTTGGCGTCATAT
                                                                                                                                                                        /product= "NIM1 protein variant 2" /note= "N-terminal deletion compared to wild-type
                                                                                                                                                                                                                                                                                                                              Non-inducible immunity-1 (NIM1) protein variant 2 encoding cDNA.
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960S-0033177.
960S-0034379.
970S-0034730.
970S-0035022.
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                                                                                                                                                                                                                                                                                                                                              Non-inducible
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27-DEC-1996;
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10-JAN-1997
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This cDNA encodes an altered form of the Arabidopsis thaliana non-
inducible immunity-1 (NIMI) protein. Sequences shown in AAV43661 to
AAV44565 represent variants of the NIMI bonA. The invention provides a
chimeric gene comprising a promoter active in plants operatively linked
confirmed with a recombinant vector comprising such a
cells stably transformed with a recombinant vector comprising such a
chimeric gene have a broad spectrum of disease resistance. The altered
confirmed resistance (SAR) signal transduction pathway. The transgenic
confirmed resistance (SAR) signal transduction pathway. The transgenic
confirmed resistance (SAR) signal transformed plants than in a wild-type
plants transformed with an altered NIMI gene exhibits constitutive SAR
expression which is higher in the transformed plants than in a wild-type
plant The products can be used for producing plants with a broad
confirmed disease resistance. Overexpression of NIMI mimics the effects
of inducer compounds that induce constitutive immunity (CIM) phenotype
confirmed inventions can be used with plants such as rice, wheat,
conficory, lettuce, cabbage, cauliflower, broccoli, turnip, radish,
conficory, lettuce, cabbage, cauliflower, broccoli, turnip, radish,
conficory, lettuce, apparagus, onion, garlic, egglant, peper, cance,
consumbly, pumpkin, zucchini, cucumber, apprapary grape, raspberry,
consumberry, peach, nectarine, apricot, strawberry, grape, raspberry,
consumberry, pincapple, avocado, papaya, mango, banana, soybean, tobacco,
contacto, sorghum and sugarcane. The plants produced are resistant to
consumptions and nematodes. The plants produced can be used
consumptions and lepidoptera and nematodes. The plants produced can be used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Use of non-inducible immunity-1 gene - for transforming plants to produce transgenic plants having a broad spectrum disease resistance
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        526 AAGGAGTTTCTGAATGCGCAGAAGTTGCTGCCACGTGGCTTGCCGGCGGCGTGG
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Pred. No. 0;
0; Mismatches
                                                                               Claim 9; Pages 149-152; 205pp; English.
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        GCAAGCATTCTCTCAAAGGCCGACTATGTGTAGAAATACTAGAGCAAGAAGACAAACGAG
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                             GGAATCCGAGGGGATATACGGTGCTTCATGTTGCTGCGATGCGGAAGGAGCCACAATTGA
                                                                                      CACTCATGATCGCAAAACAAGCCACTATGGCGGTTGAATGTAATAATACCCGGAGCAAT
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Search completed: October 7, 2002, 22:58:29 Job time: 321.819 secs

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7, 2002, 22:39:34; Search time 45.7605 Seconds (without alignments) 11293.859 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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US-08-880-179-2
US-08-980-179-1
US-08-989-478-11
US-08-986-685-11
US-08-989-478-9
US-08-989-478-13
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5-08-996-685-15
5-08-232-463-14
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Maximum Match 100%
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Maximum DB seq length: 200000000
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Sequence 13, Appl	US-08-487-826B-13	7	19124	1.7	35	45
Sequence 11, Appl	US-08-487-826B-11	7	8220	1.7	35	44
Sequence 11, Appl	US-08-568-459A-11	7	8220	1.7	35	43
Sequence 17, Appl	US-08-909-965C-17	7	1908	1.7	35	42
Sequence 2, Appli	US-09-141-000-2	r	200	1.7	35.2	41
Sequence 2, Appl	PCT-US95-16216-2	വ	10136	1.7	35.4	c 40
Sequence 2, Appl	US-08-353-700-2	<b>-</b>	10136	1.7	35.4	c 39
Sequence 5, Appl	US-08-328-254-5	Н	8789	1.7	35.4	c 38
Sequence 427, App	US-09-385-982-427	4	267	1.7	35.8	
Sequence 494, App	US-09-385-982-494	4	374	1.7	36	c 36
Patent No. 521973	5219739-16	9	961	1.7	36.4	35
Patent No. 5194596	5194596-16	9	961	1.7	36.4	34
Patent No. 5194596	5194596-8	9	790	1.7	36.4	33
Sequence 2, Appli	US-08-451-405A-2	Н	731	1.7	36.4	c 32
Sequence 476, App	US-09-439-313-476	4	3434	1.7	36.6	31
Patent No. 5219739	5219739-8	9	789	1.7	36.6	30
Sequence 353, Ap	US-09-439-313-353	4	436	1.7	36.8	c 59
Sequence 12, Appl	US-08-545-196B-12	٣	1582	1.8	37.2	28

## ALIGNMENTS

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APPLICANT: Uknes, Scott
APPLICANT: Uknes, Scott
APPLICANT: Hunt, Michelle
APPLICANT: Steiner, Henry-York
APPLICANT: Steiner, Henry-York
APPLICANT: Ryals, John
TITLE OF INVENTION: DISEASE RESISTANCE IN PLANTS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5986082artis Corporation
STREET: 3054 Coriwallis Road
CITY: Research Triangle Park
STATE: No. 5986082th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-21214/P1/CGC1911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,177
FILING DATE: 13-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,379
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,382
FILING DATE: 27-DEC-1996
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,730
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,021
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FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,022
APPLING DATE: 10-JAN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/989,478
                     Sequence 6, Application US/08989478 Patent No. 5986082 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE
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US-08-989-478-6
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llarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
                                                                                                                                      CDNA
                                                                                                                                                               LOCATION: 43..1824
OTHER INFORMATION: /product= "NIM1
                                                                                                                                       /note= "NIM1
                                                                                                   ORGANISM: Arabidopsis thaliana
TELECOMMUNICATION INFORMATION:
                         9
        TELEPHONE: (919) 541-858
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
                                          LENGTH: 2011 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                   NAME/KEY: misc_feature
LOCATION: 1..2011
OTHER INFORMATION: /not
                                                                                 CDNA
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Matches 2010; Conser
                                                                                        SOURCE:
                                                                              MOLECULE TYPE:
ORIGINAL SOURCE
                                                                                                                                                          NAME/KEY:
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                   1911 ATAATTCTGTTTTCATGATGACTGTAACTGTTTATGTCTATCGTTGGCGTCATATAGTTT 1970
                                                                                    APPLICANT: Ryals, John
APPLICANT: Friedrich, Leslie
APPLICANT: Friedrich, Leslie
APPLICANT: Wolina, Antonio
APPLICANT: Molina, Antonio
APPLICANT: Ruess, Wilhelm
APPLICANT: Knauf Beiter, Gertrude
APPLICANT: Knauf Ruth
APPLICANT: Kung, Ruth
APPLICANT: Costendorp, Michael
TITLE OF INVENTION: METHOD FOR PROTECTING PLANTS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     No. 6031153artis Corporation
                                                                                                                                                                                                  ACAATTTGAACCAATGGTATACAGATTTGTA 2061
                                                                                                                                                                                                                     APPLICATION NUMBER: US 60/034,378
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,379
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,382
FILING DATE: 27-DEC-1996
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 10-7AN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,022
FILING DATE: 10-3AN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,024
FILING DATE: 10-3AN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/761,543
FILING DATE: 6-DEC-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 60/034,730 FILING DATE: 10-JAN-1997 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 60/035,021
FILING DATE: 10-JAN-1997
                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/08996685
Patent No. 6031153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6031153th Carolina
COUNTRY: USA
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PRIOR APPLICATION DATA

APPLICATION NUMBER: US 08/875,015
FILING DATE: 16-JUL-1997
ATTONREY/AGENT INFORMATION:
NAME: Mediss, J Timothy
REGISTRATION NUMBER: 38,241
REGISTRATION NUMBER: PF/5-21215/P1/CGC1912
TELEPHONE: (919) 541-8587
TELEPHONE: (919) 541-8689
INFORMATION FOR SEO ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 2011 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: 1..2011
OTHER INFORMATION: /note= "NIM1 cDNA sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 43.1824
OTHER INFORMATION: /product= "NIM1 protein"
US-08-996-685-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

95.5%; Score 2009.4;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2010; Conservative 0; Mismatches
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MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
ORGANISM: Arabidopsis thaliana
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TYPE: nucleic acid
STRANDEDNESS: single
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REGISTRATION NUMBER:
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CITY: Re
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APPLICANT: Hunt, Michelle
APPLICANT: Steiner, Henry-York
APPLICANT: Steiner, Henry-York
TITLE OF INVENTION: ALTERED FORMS OF THE NIM1 GENE CONFERRING
TITLE OF INVENTION: DISEASE RESISTANCE IN PLANTS
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                             2031 ACAATTTGAACCAATGGTATACAGATTTGTA 2061
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/989,478
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,177
FILING DATE: 13-DEC-1996
FILING DATE: 13-DEC-1996
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FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 60/034,382
FILING DATE: 27-DEC-1996
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FILING DATE: 10-JAN-1997
ATTORNEY/AGENT INFORMATION:
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10-JAN-1997
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10-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7, Application US/08989478 Patent No. 5986082 GENERAL INFORMATION:
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Research Triangle Park
No. 5986082th Carolina
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SER: 38,241
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APPLICATION NUMBER:
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REPERENCE/DOCKET NUMBER: PF/5-21214/P1/CGC1911
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEPKX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2011 base pairs
TYPE: nucleic acid
STRANEDNESS: single
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OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: MOTHER INFORMATION: I
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                                               1801 AAACTCTCATCATCGTCGTCGTGAGACTCTTGCCTCTTAGTGTAATTTTTGCTGTACCAT
                                                                                              ATAATTCTGTTTTCATGATGACTGTAACTGTTTATGTCTATCGTTGGCGTCATATAGTTT
                                   1851 AAACTCTCTCATCGTCGTCGTGAGACTCTTGCCTCTTAGTGTAATTTTTGCTGTACCAT
                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Knauf-Beiter, Gertrude
APPLICANT: Kung, Ruth
APPLICANT: Knng, Ruth
APPLICANT: Oostendarp, Michael
TITLE OF INVENTION: METHOD FOR PROTECTING PLANTS
CORRESPONDENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6031153art1s Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/996,685
                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: No. 6031153artis Corporation STREET: 3054 Cormwalls Road CITY: Research Triangle Park STATE: No. 6031153th Carolina ZIP: USA
                                                                                                                                                                              ACAATTTGAACCAATGGTATACAGATTTGTA 2061
                                                                                                                                                                                          APPLICATION NUMBER: US 60/035,021
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 60/035,022
FILING DATE: 10-JAN-1997
                                                                                                                                                                                                                                                                                                           Friedrich, Leslie
Uknes, Scott
Molina, Antonio
Ruess, Wilhelm
Knauf-Beiter, Gertrude
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                 Sequence 7, Application US/08996685 Patent No. 6031153
                                                                                                                                                                                                                                                                                                    Ryals, John
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COMPUTER READABLE FORM:
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APPLICANT:
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/product= "altered form of NIM1"
/note= "Serine residues at amino acid positions 55 and 59
wild-type_NIM1 gene product have been changed to Alanine
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                                                                                                                                                       PF/5-21215/P1/CGC1912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 95.4%; Score 2006.2; Best Local Similarity 99.9%; Pred. No. 0; Matches 2008; Conservative 0; Mismatches
PRIOR APPLICATION DATE:

PRIDE APPLICATION NUMBER: US
FILING DATE: 10-JAN-1997

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: US 08/875,015

PTILING DATE: 16-JUL-1997

ATTORNEY/AGENT INFORMATION:

NAME: Meigs, J. Timothy

REGISTRATION NUMBER: PF/5-21215/

REPERONGE/DOCKET NUMBER: PF/5-21215/

TELEFONMUNICATION INFORMATION:

TELEFON: (919) 541-8589

INFORMATION FOR SEO ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 2011 base pairs

TYPE: nucleic acid

STRANDENNES: single
                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS.
LOCATION: 43.1824
COTHER INFORMATION: /FOCCHOOTHER INFORMATION: wild**
OTHER INFORMATION: residite
FEATURE: NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCATION: 205.217
CTHER INFORMATION:
CTHER INFORMATION:
US-08-996-685-7
                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                    linear
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	AAAGGTGCAAG AAAGGTGCAAG CAAGCCACTAT CAAGCCACTAT GGCCGACTATG GTTCCTCCCTC GTTCTTCTCTC GTTCTTCTCTCT GTTCTTCTTG GTTCTTCTTG AATAGAGTTGC AATAGAG	THILLIHILIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHI
		191 ATGATCGC 191 ATGATCGC 141 ATGATCGC 251 CATTCTCT 201 CATTCTCT 311 ATTCTAG 371 CTCGATCT 431 GCAATGGA 431 GCATTCCC 431 GACGTCT 1111111111111111111111111111111111

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1911 ATAATTCTGTTTTCATGATGACTGTAACTGTTTATGTCTATCGTTGGCGTCATATAGTTT 1970
                                                                                                                                                                                                                                                                                                                                                                        1791 TCCCTGACAGATTCGACTTCTTCCACATCGAAATCAACCGGTGGAAAGAGGGTCTAACCGT 1850
                                                                                    GAAATACAAGAGACACTAAAGAAGGCCTTTAGTGAGGACAATTTGGAATTAGGAAATTCG 1790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Uknes, Scott
APPLICANT: Hord: Michelle
APPLICANT: Hord: Michelle
APPLICANT: Steiner, Henry-York
APPLICANT: Ryals, John
TITLE OF INVENTION: ALTERED FORMS OF THE NIMI GENE CONFERRING
TITLE OF INVENTION: ALTERED FORMS OF THE NIMI GENE CONFERENCE ADDRESS:
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSE: No. 5986082artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 5986082th Carolina
COUNTRY: USA
ZIP: 27709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: EL PR PC COMPATIBLE
COMPUTER: TEM PC COMPATIBLE
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/989,478
FILING DATE:
CLASSIFICATION:
APPLICATION NUMBER: US 60/033,177
FILING DATE: 13-DEC-1996
PRIOR APPLICATION NUMBER: US 60/034,379
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,379
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,382
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,382
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1981 ACAATTTGAACCAATGGTATACAGATTTGTA 2011
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,021
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08989478 Patent No. 5986082
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US-08-989-478-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 5655,
                                                                                                                                                                                                                                    OTHER INFORMATION: /product= "1st exon of NIM1"
                                                                                                                                                                                                                                                                                                                                                                     /product= "4th exon of NIM1'
                                                        PF/5-21214/P1/CGC1911
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Pred. No. 0;
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APPLICATION NUMBER: US 60/035,022 FILING DATE: 10-JAN-1997 ATTORNEY/AGENT INFORMATION:
                              NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REPRENCE/DOCKET NUMBER: PF/5-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8689
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5655 base pairs
                                                                                                                                                                                                                                                           NAME/KEY: exon
LOCATION: 3427..4162
OTHER INFORMATION: /product=
                                                                                                                                                                                                                                                                                                               LOCATION: 4271..4474
OTHER INFORMATION: /product=
                                                                                                                                                       TOPOLOGY: linear
MOLEGULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRATURE:
NAME/KEY: excn
LOCATION: 2787.3347
                                                                                                                                                                                                                                                                                                                                                                                                                                      83.7%;
87.5%;
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Matches 2088; Conservative
                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                              NAME/KEY: exon
LOCATION: 4586..486
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                     NAME/KEY: exon
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; LOCATION:
US-08-989-478-1
                                                                                                                                                                                                                                               FEATURE:
NAME/KEY:
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3714 1241 3474 3654 3954 3115 TGAAGCTCGAGCTTAAGGAGATTGCCAAGGATTACGAAGTCGGTTTCGATTCGGTTGTGA 3174 1002 GCATATTGCAATGTGAAGACCGCAACAGATCTTTTAAAACTTGATCTTGCCGATGTCAAC 1061 821 881 941 761 3895 TIGATACTATCTCTATIGGAAAAAGGTGCAAGTGCATCAGAAGCACATTGGAAGGTAGA **ACCGCACTCATGATCGCAAAACAAGCCACTATGGCGGTTGAATGTAATAATATCCCGGAG** CTGTTTTGGCTTATGTTTACAGCAGCAGAGTGAGACCGCCGCCTAAAGGAGTTTCTGAAT ACCATCTGCATTAAAGCTATGGTTACACATTCATGAATATGTTCTTACTTGAGTACTTGTA -----TCAGAGGCACTTATTGGACGTTGTAGACAAAGTTGTTATAGAGGACACATTG AAAGAGATTATTGTCAAGTCTAATGTAGATATGGTTAGTCTTGAAAAGTCATTGCCGGAA GAGCTTGTTAAAGAGATAATTGATAGACGTAAAGAGCTTGGTTTGGAGGTACCTAAAGTA AAGAAACATGTCTCGAATGTACATAAGGCACTTGACTCGGATGATATTGAGTTAGTCAAG TTGCTTTTGAAAGAGGATCACACCAATCTAGATGATGCGTGTGTCTTCATTTCGCTGTT CATAGGAATCCGAGGGGATATACGGTGCTTCATGTTGCTGCGATGCGGAAGGAGCCACAA TTGATACTATCTCTATTGGAAAAAGGTGCAAGTGCATCAGAAGCAACTTTGGAAGGTAGA CAATGCAAGCATTCTCTCAAAGGCCGACTATGTGTAGAAATACTAGAGCAAGAAGACAAA CGAGAACAAATTCCTAGAGATGTTCCTCCTCTTTTGCAGTGGCGGCCGATGAATTGAAG ATGACGCTGCTCGATCTTGAAAATAG------

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CURENTING STSIEM: PC-DOS/MS-DOS
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,685
FILING DATE: US/08/996,885
FILING DATE: US/08/996
FILING DATE: US/08/996
FILING DATE: Z1-DEC-1996
FILING DATE: Z2-DEC-1996
FILING DATE: Z1-DEC-1996
FILING DATE: US/034,382
FILING DATE: US/034,382
FILING DATE: US/034,382
FILING DATE: US/034,382
FILING DATE: US/034,390
FILING DATE: US/034,390
FILING DATE: US/034,390
FILING DATE: US/035,021
FILING DATE: US/035,022
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OTHER INFORMATION: /Product= "3rd exon of NIM1"
FEATURE:
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OTHER INFORMATION: /product= "1st exon of NIM1"
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OTHER INFORMATION: /product= "2nd exon of NIM1"
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NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSE: No. 6031153artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6031153th Carolina
COUNTRY: USA
ZIP: 27709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,024
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/875,015
FILING DATE: 16-JUL-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Meigs, J. Timothy
REGIETRATION UNUBER: 38,241
REFRENCE/DOCKET NUMBER: PF/5
TELECOMMUNICATION INFORMATION:
TELEPAN: (919) 541-8587
TELEFAX: (919) 541-8699
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 5655 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                 COMPUTER READABLE FORM:
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                                      1494 CGTCTCACTGGTACGAAGAGAACATCACCGGGTGTAAAGATAGCACCTTTCAGAATCCTA 1553
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                                                                                                                                                                                                                                                                                                                                                                                                                         --------GTGGAACTCGGGAAACGATTCTTCCCGCGC
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APPLICANT: Kush
APPLICANT: Kesmann, Helmut
APPLICANT: Oostendorp, Michael
TITLE OF INVENTION: METHOD FOR PROTECTING PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08996685
Patent No. 6031153
GENERAL INFORMATION:
APPLICANT: Friedrich, Leslie
APPLICANT: Willes, Scott
APPLICANT: Mollan, Antonio
APPLICANT: Mollan, Antonio
APPLICANT: Kness, Wilhelm
APPLICANT: Knauf-Beiter, Gertrude
APPLICANT: Knuf, Ruth
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                                           join(2787..3347, 3427..4162, 4271..4474, 4586..4866)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 5655;
                                                                                      Indels
                 of NIM1
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0
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                                                                    DB
                                                                  Score 1760; DE Pred. No. 0; 0; Mismatches
        LOCATION: 4586..4866
OTHER INFORMATION: /product= "4th exon
FEATURE:
                                                                   83.7%;
87.5%;
                                                                                      Conservative
                                                                            Best Local Similarity
Matches 2088; Conserv
                                  CDS
                                 ; NAME/KEY:
; LOCATION:
US-08-996-685-1
NAME/KEY:
                                                                     Query Match
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4614 1361 GAAGACGACACTGCTGAGAAACGACTACAAAAGAAGCAAAGGTACATGGAAATACAAGAG 1742 1181 3954 ATGGAGATCGCCGAAATGAAGGGAACATGTGAGTTCATAGTGACTAGCCTCGAGCCTGAC 1493 CAATGCAAGCATTCTCTCAAAGGCCGACTATGTGTAGAAATACTAGAGCAAGAAGAAAA 1301 TGCTGTCTGACCTTGTTTTTTTTTTTTATCACGGAAACGGGAAACGATTCTTCCCGCGC TGTTCGGCAGTGCTCGACCAGATTATGAACTGTGAGGACTTGACTCAACTGGCTTGCGGA TIGCITITIGAAAGAGGATCACACCAATCIAGAIGAIGCGIGIGCCICTICAITICGCIGIT **ACCGCACTCATGATCGCAAAACAAGCCACTATGGCGGTTGAATGTAATAATATCCCGGAG** CGAGAACAAATTCCTAGAGATGTTCCTCCTCTTTTGCAGTGGCGGCCGATGAATTGAAG AATTAAATTTATGTCCTCTCTATTAGGAAACTGAGTGAACTAATGATAACTATTCTTTGT ------AGTTGCACTTGCTCAACGTCTTTTTCCAACGGAAGCACAAGCTGCA CGTCTCACTGGTACGAAGAACATCACCGGGTGTAAAGATAGCACCTTTCAGAATCCTA CATCGGACTCCTTATCACAAAAACAAAACTAAATGATCTTTAAAACATGGTTTTGTTACT GCATATTGCAATGTGAAGACCGCAACAGATCTTTTAAAACTTGATCTTGCCGATGTCAAC TTGATACTATCTCTATTGGAAAAAGGTGCAAGTGCATCAGAAGCAACTTTGGAAGGTAGA AAGAAACATGTCTCGAATGTACATAAGGCACTTGACTCGGATGATATTGAGTTAGTCAAG GAAGAGCATCAAAGTAGACTAAAAGCGCTTTCTAAAACC-ATGACGCTGCTCGATCTTGAAAATAG-----942 3895 4015 1362 4195 4255 4315 4375 4435 1593 4495 4555 1623 4615 1683 3835 1182 1242 1302 1388 1434 1494 1554 1593 3655 1002 1062 1122 3955 4075 4135 1388 3595 3775 882 g q qq g ò δy qq Ω qq δ g δy g Óλ Q Ω g οy Ω Qγ g δy ΩD οy g ò g óλ Q δ qq Qγ ò ò ò

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OTHER INFORMATION: /product= "4th exon of NIM1"
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0; Mismatches
                                                                                                                         exon
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Best Local Similarity 87.5%; Pred. No. 0;
Matches 2088; Conservative 0; Mismatches
                                                                                                                                                                                                                                      LOCATION: 4271...4474
OTHER INFORMATION: /product= "3rd
                                                                                                                     OTHER INFORMATION: /product= "1st
                                                                                                                                                                                       OTHER INFORMATION: /product= "2nd
                      DNA (genomic)
                                                                                    NAME/KEY: exon
LOCATION: 2787..3347
                                                                                                                                                     NAME/KEY: exon
LOCATION: 3427..4162
        TOPOLOGY: linear MOLECULE TYPE: DNA
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NAME/KEY: exon
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; LOCATION: joir
US-08-880-179-2
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                                    HYPOTHETICAL:
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APPLICANT: Friedrich, Leslie
APPLICANT: Weynann, Kristianna
APPLICANT: Lawton, Kay
APPLICANT: Jawton, Kay
APPLICANT: Jawton, Kay
APPLICANT: Jawton, Kay
APPLICANT: Jawton, Kay
APPLICANT: Jeser
APPLICANT: Jeser
TITLE OF INVENTION: GENE ENCODING A PROTEIN INVOLVED IN THE
TITLE OF INVENTION: IN PLANTS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                             TCGACTICTICCACATCGAAATCAACCGGTGGAAAGAGGTCTAACCGTAAACTCTCTCAT 1862
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4675 GAAGACGACACTGCTGAGAAACGACTACAAAAGAAGCAAAGGTACATGGAAATACAAGAG 4734
                                                                                                                                                               CGTCGTCGGTGAGACTCTTGCCTCTTAGTGTAATTTTTGCTGTACCATATAATTCTGTTT 1922
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                             1743 ACACTAAAGAAGGCCTTTAGTGAGGACAATTTGGAATTAGGAAATTCGTCCCTGACAGAT
                                                1983 IGCATCCIGIGIATTATIGCIGCAGGIGIGCTICAAACAAAIGIIGIAACAAITIGAACC
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: No. 6091004artis Corporation
STREET: 520 White Plains Road, P.O. Box 2005
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ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timochy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: GGC 1909
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8689
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTER/STICS:
LENGTH: 5655 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Patent No. 6091004
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STATE: New York
COUNTRY: USA
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Sequence 1, Application US/08880179
Fatent No. 6091004
GENERAL INFORMATION:
APPLICANT: Ryals, John
APPLICANT: Fieldrich, Leislie
APPLICANT: Belancy, Terry
APPLICANT: Lawton, Kay
APPLICANT: Jesse, Taco
APPLICANT: Jesse, Jesse, Taco
APPLICANT: Jesse, Taco
APPLICANT: Jesse, Jesse, Taco
APPLICANT: Jesse, Jesse

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Version #1.30
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Pred. No. 0;
0; Mismatches
      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,179
PatentIn Release #1.0,
                   FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Melgs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/CDOCKET NUMBER: GGC TELECOMMUNICATION INFORMATION:
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 9919 base pairs
TYPE: nucleic acid
STRANBEDRESS: single
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                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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Best Local Similarity 87.5%;
Matches 2088; Conservative
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US-08-880-179-1
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                                                                                                                 1683 GAAGACGACACTGCTGAGAAACGACTACAAAAGAAGCAAAGGTACATGGAAATACAAGAG
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Patent No. 5986082
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Winch, Michelle
APPLICANT: Ryals, John
TITLE OF INVENTION: ALTERED FORMS OF THE NIMI GENE CONFERRING
TITLE OF INVENTION: DISEASE RESISTANCE IN PLANTS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                     2043 AATGGTATACAGATTTGTAATATATATTTATGTACATCAACAATAA 2088
                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/989,478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: No. 5986082artis Corporation STREET: 3054 Cornwallis Road CITY: Research Triangle Park STATE: No. 5986082th Carolina COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,177
FILING DATE: 13-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 27709
COMPUTER READABLE FORM:
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/product= "Altered form of NIM1" /note= "C-terminal deletion compared to wild-type NIM1."
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100.0%; Pred. No. 0;
Live 0; Mismatches
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/034,379
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,382
FILING DATE: 27-DEC-1996
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,730
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,021
FILING DATE: 10-JAN-1997
PRIOR APPLICATION NUMBER: US 60/035,021
FILING DATE: 10-JAN-1997
FILING DATE: 10-JAN-1997
ATTORNEY AGENT INFORMATION:
ATTORNEY AGENT INFORMATION:
ATTORNEY AGENT INFORMATION:
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                 NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5
TELECOMUNICATION INFORMATION:
TELEPHONE: (919) 541-8687
TELERAX: (919) 541-8687
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 1608 base pairs
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Best Local Similarity 100.9
Matches 1605; Conservative
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STRANDEDNESS: single
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; OTHER INFORMATION:
; OTHER INFORMATION: ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: CDNA
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us-08-908-884-2.rni

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1561 TTCTTCCCGCGCTGTTCGGCAGTGCTCGACCAGATTATGAACTGT 1605
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APPLICATION NUMBER: 1
                                                                                       Ryals, John
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APPLICATION NUMBER:
                                                                         GENERAL INFORMATION:
APPLICANT: Ryals,
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                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                          APPLICANT:
APPLICANT:
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APPLICANT:
                                  RESULT 10
US-08-996-685-11
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                                                                  Patent No.
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                                  CAGAGGCACTTATTGGACGTTGTAGACAAAGTTGTTATAGAGGACACATTGGTTATACTC
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APPLICANT: Kessmann, Helmut
APPLICANT: Oostendorp, Michael
TITLE OF INVENTION: METHOD FOR PROTECTING PLANTS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: No. 6031153artis Corporation STREET: 3054 Cornwallis Road CITY: Research Triangle Park STATE: No. 6031153th Carolina COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/761,543
FILING DATE: 6-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,378
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,379
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 27-DEC-1996
FRIOR APPLICATION DATE:
APPLICATION NUMBER: US 60/034,730
FILING DATE: 10-43A-1997
FRIOR APPLICATION DATE:
APPLICATION NUMBER: US 60/035,021
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATE: US 60/035,021
FRICR APPLICATION DATE: US 60/035,022
FILING DATE: 10-JAN-1997
FILING DATE: 10-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/996,685
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                                                                                                                                                             Ruess, Wilhelm
Knauf-Beiter, Gertrude
Kung, Ruth
Kessmann, Helmut
Sequence 11, Application US/08996685
Patent No. 6031153
                                                                                                                                                                                                                                                                                                                                                                                                                               USA
21P: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MC
SOFTWARE: Patent
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REFERENCE/DOCKET NUMBER: PE,
TELECOMMUNICATION INFORMATION:
                                                                                           Friedrich, Leslie
Uknes, Scott
Molina, Antonio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (919) 541-8587
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (919) 541-8689 INFORMATION FOR SEQ ID NO: 1 SEQUENCE CHARACTERISTICS:
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ATTCCTAGAGATGTTCCTCCTCTTTTGCAGTGGCGGCCGATGAATTGAAGATGACGCTG 1370
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                                                                                                             CTCGATCTTGAAAATAGAGTTGCACTTGCTCAACGTCTTTTTCCAACGGAAGCACAAGGT
CATTCTCTCAAAGGCCGACTATGTGTAGAAATACTAGAGCAAGAAGACAAACGAGAACAA
                                                                                   1021 CCGAGGGGATATACGGTGCTTCATGTTGCTGCGGATGCGGAAGCGAAGCACAATTGATACTA
                                                                                                                                                  ATGATCGCAAAACAAGCCACTATGGCGGTTGAATGTAATAATATCCCGGAGCAATGCAAG
                                                                                                                                                             AATGTGAAGACCGCAACAGATCTTTTAAAACTTGATCTTGCCGATGTCAACCATAGGAAT
                                              1071 CCGAGGGGATATACGGTGCTTCATGTTGCTGCGATGCGGAAGGAGCCACAATTGATACTA
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APPLICANT: Hunt, Michelle
APPLICANT: Hunt, Michelle
APPLICANT: Steiner, Henry-York
APPLICANT: Ryals, John
TITLE OF INVENTION: DISEASE RESISTANCE IN PLANTS
TITLE OF INVENTION: DISEASE RESISTANCE IN PLANTS
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5986082artis Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                      1611 TICTICCCGCGCTGTTCGGCAGTGCTCGACCAGATATGAACTGT 1655
                                                                                                                                                                                                                                                                                                                                                                                                                                1561 TICTTCCCCCCCTTTCGCCAGTGCTCGACCAGATTATGAACTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEE: No. 5986082artis Corporation
: 3054 Cornwallis Road
Research Triangle Park
No. 5986082th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PE: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-989-478-9; Sequence 9, Application US/08989478; Patent No. 5986082; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 27709
COMPUTER READABLE FORM:
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COMPUTER: IBM
OPERATING SYST
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                                                                                         1608;
                                                     /product= "Altered form of NIM1" /note= "C-terminal deletion compared
                                                                                                           Indels
                                                                                         Length
                                                    form of NIM1"
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                                                                                          DB
                                                                                        Ouery Match
76.3%; Score 1605; E
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1605; Conservative 0; Mismatches
single
                                  NAME/KEY: CDS
LOCATION: 43..1608
OTHER INFORMATION: ,
       TOPOLOGY: linear MOLECULE TYPE: CDNA
STRANDEDNESS:
                                                                         US-08-996-685-11
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PatentIn Release #1.0, Version #1.30
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99.9%; Pred. No. 0;
iive 0; Mismatches
                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,730
FILING DATE: 10-7AN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,021
FILING DATE: 10-7AN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,022
FILING DATE: 10-7AN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                              APPLICATION NUMBER: US 60/034,379 FILING DATE: 27-DEC-1996
                     US/08/989,478
                                                                                                                                US 60/034,382
                                                                 60/033,177
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                                                                                                                                                                                                                                                                 NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKT NUMBER: PF
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1597 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                              APPLICATION NUMBER: US 6C FILING DATE: 13-DEC-1996 PRIOR APPLICATION DATA:
                                                                                                         FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 66
FILING DATE: 27-DEC-1996
                                                                                                                                                                                                                                                                                                               (919) 541-8587
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Best Local Similarity 99.9
Matches 1594; Conservative
          DATA:
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OTHER INFORMATION:
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LOCATION:
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Query Match
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1502 AGTTTCGCTCTTCGTTTTGCATCCTGTGTATTATTGCTGCAGGTGTGCTGCAACAAAAAAG 1561
                                              Oostendorp, Michael
VENTION: METHOD FOR PROTECTING PLANTS
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                                                                                                                                   2026 TIGIAACAATTIGAACCAATGGIATACAGATTIGIA 2061
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PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/761,543
FILING DATE: 6-DEC-1996
PRIOR APPLICATION NUMBER: US 60/034,378
FILING DATE: 27-DEC-1996
FILING DATE: 10-0704,382
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APPLICATION DATA:
APPLICATION NUMBER: US 08/875,015
FILING DATE: 16-UUL-1997
ATTORNEY AGENT INFORMATION:
NAME: Meigs, J. Timothy
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APPLICATION NUMBER: US 60/035,022
FILING DATE: 10-JAN-1997
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Uknes, Scott
Molina, Antonio
Ruess, Wilhelm
Knauf-Beiter, Gertrude
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FILING DATE: 10-JAN-1997
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FILING DATE: 10-JAN-1997
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                               Sequence 9, Application US/08996685 Patent No. 6031153
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APPLICANT: Kessmann, Helmut
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CORRESPONDENCE ADDRESS:
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APPLICANT: Ryals,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  766 AGATTATTGTCAAGTCTAATGTAGATATGGTTAGTCTTGAAAAGTCATTGCCGGAAGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         886 AACATGTCTCGAATGTACATAAGGCACTTGACTCGGATGATATTGAGTTAGTCAAGTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1006 ATTGCAATGTGAAGACCGCAACAGATCTTTAAAAACTTGATCTTGCCGATGTCAACCATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGAATCCGAGGGGATATACGGTGCTTCATGTTGCTGCGATGCGGAAGGAGCCACAATTGA
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0
                                                                                                                                                                                                                                                                                                                                                                                  Length 1597
                                                                                                                                                                                                                                                                                                                                                                                  DB 3;
38,241
RR: PF/5-21215/P1/CGC1912
                                                                                                                                                                                                                                                                                                                                                                                                                     5;
                                                                                                                                                                                                                                                                                                                                                                                Score 1592.8;
                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 0;
               REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1597 base pairs
                                                                                                                                                                                                                                                                                                                                                                                75.7%;
                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 99.9
Matches 1594; Conservative
     REGISTRATION NUMBER:
                                                                                                                                                      nucleic acid
                                                                                                                                                                                                                                                                  LOCATION: 1..1410
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                         CTHER INFORMATION:
US-08-996-685-9
                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                      TYPE: nucleic STRANDEDNESS:
                                                                                                                                                                                                                               FEATURE:
NAME/KEY: CDS
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466 TCGATTCGGTTGTGACTGTTTTGGCTTATGTTTACAGCAGCAGAGTGAGACCGCCGCCCTA 525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product= "Altered form of NIM1"
/note= "N-terminal/C-terminal chimera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                              Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: PF/5-21214/P1/CGC1911
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8689
INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56.5%; Score 1188.4; 99.9%; Pred. No. 0; iive 0; Mismatches
                       Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 60/034,730
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,021
FILING DATE: 10-JAN-1997
PRIOR APPLICATION NUMBER: US 60/035,022
FILING DATE: 10-JAN-1997
ATTORNEY, AGENT INFORMATION:
                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,177
FILING DATE: 13-DEC-1996
PRIOR APPLICATION NUMBER: US 60/034,379
FILING DATE: 27-DEC-1996
PRIOR APPLICATION NUMBER: US 60/034,382
FILING APPLICATION DATA:
APPLICATION NUMBER: US 60/034,382
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,730
APPLICATION NUMBER: US 60/034,730
                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/989,478
STREET: 3054 Cornwallis Road CITY: Research Triangle Park STATE: No. 5986082th Carolina ZIP: 7770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Meigs, J. Timothy REGISTRATION NUMBER: 38,241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 1194 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 99.9
Matches 1189; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
LOCATION: 1..1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                              27709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-989-478-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                   1486 AGCCTGACCGTCTCACTGGTACGAAGAACATCACCGGGTGTAAAGATAGCACCTTTCA 1545
                                                                                                                                                                                                                                                                                                                                                                                              1022 AGCCTGACCGTCTCACTGGTACGAAGAGAACATCACCGGGTGTAAAGATAGCACCTTTCA 1081
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1725
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1786 ATTCGTCCCTGACAGATTCGACTTCTTCCACATCGAAATCAACCGGTGGAAAGAGGTCTA 1845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1322 ATTGECCEGACAGATEGACTECTECCACATGAAATCAACGGTGGAAAGAGGTCTA 1381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1846 ACCGTAAACTCTCCTCATCGTCGTCGTGAGACTCTTGCCTCTTAGTGTAATTTTTGCTGT 1905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCATATAATTCTGTTTTCATGATGACTGTAACTGTTTATGTCTATCGTTGGCGTCATAT 1965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1366 CGCTGCTCGATCTTGAAATAGAGTTGCACTTGCTCAACGTCTTTTTCCAACGGAAGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1666 CTCAACTGGCTTGCGGAGAAGACGACACTGCTGAGAAACGACTACAAAAGAAGCAAAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Unes, Scott
APPLICANT: Hunt, Michelle
APPLICANT: Hunt, Michelle
APPLICANT: Steiner, Henry-York
APPLICANT: Steiner, Henry-York
APPLICANT: Syals, John
TITLE OF INVENTION: ALTERED FORMS OF THE NIM1 GENE CONFERRING
TITLE OF INVENTION: DISEASE RESISTANCE IN PLANTS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2026 ITGTAACAATTTGAACCAATGGTATACAGATTTGTA 2061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 13, Application US/08989478 Patent No. 5986082 GENERAL INFORMATION:
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Molina, Antonio Ruess, Wilhelm Knauf-Beiter, Gertrude

Uknes, Scott

Kessmann, Helmut

Kung, Ruth

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APPLICANT: Oostendorp, Michael TITLE OF INVENTION: METHOD FOR PROTECTING PLANTS NUMBER OF SEQUENCES: 32
                                                                                                                                                                                              CORRESPONDENCE ADDRESS: ADDRESSEE: No. 6031153artis
                                    APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                      APPLICANT
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                                                                                                                                                                                                                                                                                                                                                                        946 TTTTGAAAGAGGATCACCAATCTAGATGATGCGTGTGCTCTTCATTTCGCTGTTGCAT 1005
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1006 ATTGCAATGTGAAGACCGCAACAGATCTTTTAAAACTTGATCTTGCCGATGTCAACCATA 1065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1056 GGAATCCGAGGGGATATACGGTGCTTCATGTTGCTGCGATGCGGAAGGAGCCACAATTGA 1125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1126 TACTATCTCTATTGGAAAAGGTGCAAGTGCATCAGAAGCAACTTTGGAAGGTAGAACCG 1185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1306 AACAAATTCCTAGAGATGTTCCTCCTTTTTGCAGTGGCGGCCGATGAATTGAAGATGA 1365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1082 GAATCCTAGAAGAGCATCAAAGTAGACTAAAAGCGCTTTCTAAAACCGTGGAACTCGGGA 1141
                                                                                                          825
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                                                                                                                                                                                                                     301
                                                                                                                                                   361
                    706 TACTCAAGCTTGCTAATATATGTGGTAAAGCTTGTATGAAGCTATTGGATAGATGTAAAG
                                             826 TTGTTAAAGAGATAATTGATAGACGTAAAGAGCTTGGTTTGGAGGTACCTAAAGTAAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                 482 TTTTGAAAGAGGATCACACCAATCTAGATGATGCGTGTGCTCTTCATTTCGCTGTTGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1246 GCAAGCATTCTCTCAAAGGCCGACTATGTGTAGAAATACTAGAGCAAGAAAAAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1486 AGCCTGACCGTCTCACTGGTACGAAGAGAACATCACCGGGTGTAAAGATAGCACCTTTCA
                                                                                                          766 AGATTATTGTCAAGTCTAATGTAGATATGGTTAGTCTTGAAAAGTCATTGCCGGAAGAGC
                                                                                                                                                                                                                                                                                    886 AACATGTCTCGAATGTACATAAGGCACTTGACTCGGATGATATTGAGTTAGTCAAGTTGC
                                                                                                                                 1606 AACGATTCTTCCCGCGCTGTTCGGCAGTGCTCGACCAGATTATGAACTGT 1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1142 AACGATTCTTCCCGCGCTGTTCGCCAGTGCTCGGCAGATTATGAACTGT 1191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
US-08-996-685-13
Sequence 13, Application US/08996685;
Patent No. 6031153
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               962
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/note= "N-terminal/C-terminal chimera."
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                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-21215/P1/CGC1912
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FELLAND DATE:

PRIOR APPLICATION NUMBER: US 60/034,378
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,379
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,382
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,730
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,021
FILING DATE: 10-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/875,015
FILING DATE: 16-JUL-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/761,543
FILING DATE: 6-DEC-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,024
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/996,685
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6031153th Carolina
COUNTRY: USA
                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1194 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTHER INFORMATION: /
COTHER INFORMATION: /
COTHER INFORMATION: /
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                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: li
                                                                                             27709
                                                                                                                                                                                                                                                                                         FILING DATE:
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APPLICANT: Ryals, John APPLICANT: Friedrich, Leslie

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1022 AGCCTGACCGTCTCACTGGTACGAGAGAACATCACCGGGTGTAAAGATAGCACCTTTCA 1081
                                                                           1082 GAATCCTAGAAGAGCATCAAAGTAGACTAAAAGCGCTTTCTAAAACCGTGGAACTCGGGA
                                               GAATCCTAGAAGAGCATCAAAGTAGACTAAAAGCGCTTTCTAAAACCGTGGAACTCGGGA
                                                                                                                                                                                                                                             ENERAL INFORMATION:
APPLICANT: Unnes, Scott
APPLICANT: Unchelle
APPLICANT: Steiner, Henry-York
APPLICANT: Steiner, Henry-York
APPLICANT: Ryals, John
TITLE OF INVENTION: ALTERED FORMS OF THE NIMI GENE CONFERRING
TITLE OF INVENTION: DISEASE RESISTANCE IN PLANTS
TITLE OF INVENTION: DISEASE RESISTANCE IN PLANTS
                                                                                                                        1142 AACGATTCTTCCCGCGCTGTTCGCCAGTGCTCGACAGATTATGAACTGT 1191
                                                                                                         1606 AACGATTCTTCCCCCCCTGTTCGGCAGTGCTCGACCAGATTATGAACTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF/5-21214/P1/CGC1911
                                                                                                                                                                                                                                                                                                                                                              AUDRESSEE: No. 5986082artis Corporation STREET: 3054 Cornwallis Road CITY: Research Triangle Park STATE: No. 5986082++
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 60/034,379 FILING DATE: 27-DEC-1996 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 60/034,382 FILING DATE: 27-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 60/034,730 FILING DATE: 10-JAN-1997 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,021 FILING DATE: 10-JAN-1997 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,177
FILING DATE: 13-DEC-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US 60/035,022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/989,478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                               Sequence 15, Application US/08989478 Patent No. 5986082 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (919) 541-8587
TELEPAX: (919) 541-8689
INFORMATION FOR SED ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 786 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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REGISTRATION NUMBER: 38,241
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ATTORNEY/AGENT INFORMATION:
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COMPUTER READABLE FORM:
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APPLICATION NUMBER:
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CLASSIFICATION:
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 Length 1194;
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                               Indels
                               1;
 DB 3;
56.5%; Score 1188.4; 99.9%; Pred. No. 0;
                             0; Mismatches
                               Conservative
               Similarity
                            Matches 1189;
 Query Match
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                                                       Length 786;
                                                                         Indels
                   /product= "Altered form of NIM1"
/note= "Ankyrin domains of NIM1."
                                                      Query Match 37.1%; Score 781.4; DB 2; Best Local Similarity 99.9%; Pred. No. 3.3e-213; Matches 782; Conservative 0; Mismatches 1;
HAME/KEY: CDS
CCATION: 1..786
COCATION: OTHER INFORMATION:
COTHER INFORMATION:
US-08-989-478-15
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Search completed: October 8, 2002, 01:23:14 Job time : 117.761 secs

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October 7, 2002, 21:32:09; Search time 1642.95 Seconds (without alignments) 17284.510 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                  13736207 seqs, 6748477542 residues
                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                  OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	AV551266 AV551266	A1997958 701671677			BH525927 BOGTO04TF	ВН602085 ВОНКВ84ТР	T22612 4620 Lambda	BH211724 SALK 0065	AW160235 EST290093	BG464249 EM1 71 D1	BM111027 EST558563		ВН602094 ВОНКВ84ТВ		_	Œ	BG526766 63-52 Ste
SUMMARIES	QI	AV551266	AI997958	AA395706	AV557971	BH525927	BH602085	T22612	BH211724	AW160235	BG464249	BM111027	BG124935	BH602094	BG598808	BE493178	AW399343	BG526766
	DB	σ	σ	Q	φ	12	12	10	12	6	10	10	10	12	10	10	6	10
	Match Length DB	573	495	470	338	772	799	258	463	613	614	700	654	785	299	455	450	744
% Query	Match	27.2	23.4	18.0	14.6	14.5	11.2	11.0	10.9	10.1	10.0	8.9	8.9	8.5	7.8	7.6	7.3	7.3
	Score	573	493	378.6	307.8	305.2	236	231.2	228.8	212.8	211.4	187.8	186.8	172.2	163.2	160.6	154.2	152.8
Result	No.	1	c 0	m	C 4	c S	9 U	7	ထ	σ υ	10	11	12	13	14	15	16	17

27.2%; Score 573; DB 9; Length 573; 100.0%; Pred. No. 9.5e-99;

Query Match Best Local Similarity

145         6.9         629         12         B26306         B26306         F369         AW745943         BAW745943         BW745943         BW745949         BW745747         BW74769         BW7521476         BW7521476         BW7521476         BW7521476         BW7521476         BW7521476         BW7521476         BW7521476         BW7521477         BW75214	ALIGNMENTS  AV551266 Av551266 Arabidopsis thaliana roote CDNA clone R2123e05R 5', mRNA seque AV551266.1 GI:8722679 EST. thale cress. Av51266.1 GI:8722679 EST. thale cress. Av51266.1 GI:8722679 EST. thale cress. Av51266.1 GI:8722679 ENATOORSIS thaliana ENATOORSIS thaliana Arabidopsis thaliana Enatophyta; Magnollophyta; eudic Rosidae; eurosida II; Brassicales; I (Dases I to 573 I Asamizu.E., Nakamura,Y., Sato,S. ar A large scale analysis of cDNA in P A large scale analysis of cDNA in P of 12,028 non-redundant expressed size-selected CDNA libraries DNA Res. 7, 175-180 (2000) Contact: Erika Asamizu The First Laboratory for Plant Gene The	181 a 104 c 137 g 151 t
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT 1 AV551266 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM AUTHORS TITLE JOURNAL MEDLINE COMMENT FEATURES FEATURES	BASE COUNT ORIGIN

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/clone_lib="A. thaliana, Columbia Col-0, rosette-1"
/tissue_type="rosette"
/dev_stage="4 - 7 weeks"
/dev_stage="4 - 7 weeks"
/dev_stage="4 - 7 weeks"
/note="voctor: pSPORT: Site_1: Not!: Site_2: Sall: cDNA
library was derived from untreated rosette tissue from
Arabidopsis thaliana, Columbia Col-0, at 4 - 7 weeks.
Plants were grown in 1:1:1 bear moss/vormiculite/perlite
soil at 22 deg. C +/- 3 deg. C under constant light, and
watered with fertilizer. cDNA synthesis was initiated
using a Not!-oligo(dT) primer. Double-stranded cDNA was
blunted, ligated to Sall adaptors, digested with Not!,
size-selected, and cloned into the Not! and Sall sites of
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Arabidopsis thaliana
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99.6%; Pred. No. 1.4e-83;
iive 0; Mismatches 2;
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/cultivar="Columbia Col-0"
/db_xref="taxon:3702"

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Chen, J., Momityama, M., Chan, E., Mooney, M., Carroon, B., Gilliland, D., Wang, X., Hillman, J., Guegler, K., Kim, C., Doyle, M., Brzoska, P., Gorgone, G., Burns, D., Gifffin, J., Mouanoutoua, M., Nquyen, D., Tan, R., Rose, M., Warren, B., Ton, B., Kastury, K., Borillo, C., Carpio, T., Policky, J., Suzuki, G., Argentine, C., Shah, S., Nobriga, A., Murry, L., Arabidopsis thaliana Gene Expression MicroArray Unpublished (1999)

Contact: David Smoller, Ph.D.

Genome Systems, Inc., a wholly owned subsidiary of Incyte
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                                                                                                                                                                                                                                                                          AGGATCACACCAATCTAGATGATGCGTGTGTCTTCATTTCGCTGTTGCATATTGCAATG 1014
                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGGATATACGGTGCTTCATGTTGCTGCGATGCGGAAGGAGCCACAATTGATACTATCTC 1134
                                                                                                                                                                                                                                                                                                 241 TGAAGACCGCAACAGATCTTTTAAAACTTGATCTTGCCGATGTCAACCATAGGAATCCGA 300
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                                      TCAAGTCTAATGTAGATATGGTTAGTCTTGAAAAGTCATTGCCGGAAGAGCTTGTTAAAG 834
                                                                                                                                      61 AGATAATTGATAGACGTAAAGAGCTTGGTTTGGAGGTACCTAAAGTAAAGAAACATGTCT 120
                                                                                                                                                                                                                   121 CGAATGTACATAAGGCACTTGACTCGGATGATATTGAGTTGAGTTGCTTTTGAAAG 180
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Gaps
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  Mismatches
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Email: service@genomesystems.com.
Location/Qualifiers
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4633 World Parkway Circle, St.
Trel: 877-577-2733
Fax: 314-427-3324
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Arabidopsis thaliana
  Conservative
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us-08-908-884-2.rst

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Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S. A large scale analysis of CDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and DNA Res. 7, 175-180 (2000)
                                                                                         AV557971 Arabidopsis thaliana green siliques Columbia Arabidopsis thaliana green siliques Columbia Arabidopsis thaliana cDNA clone SQ085f0lF 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSS 13-DEC-2001
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="Columbia"
/db_xref="taxon:3702"
/clone="SQO85101F"
/clone_lib="Arabidopsis thaliana green siliques Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               //issue_type="green siliques"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI"
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Kazusa DNA Research Institute
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/organism="Arabidopsis thaliana"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not; Lambda PRL2 is a cDNA library derived from equal quantities of 4 pools of mRNA. The mRNA sources were 1) 7 day germinated etiolated seedlings; 2) tissue culture grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark-rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and siliques. The vector is BRL's lambda Zip-Lox. The cDNA linears were directionally cloned with Sal-Not arms using
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 470)
Newman,T., deBruijn,F.J., Green,P., Keegstra,K., Kende,H., McIntosh,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomashow,M., Retzel,E. and Somerville,C.
                                                                                                                              clones
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large-scale partial sequencing of anonymous Arabidopsis cDNA (Plant Physiol. 106, 1241-1255 (1994)
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Michigan State University
MSU-DOE PRL, Michigan State University, Plant Biology Bldg.,E.
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                                                                                                                                                                                                                                                                                                                                                                      /organism="Arabidopsis thaliana"
/strain="var columbia"
/db_xref="taxon:3702"
/clone="9905XP"
/clone_lib="Lambda-PRL2"
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                                                                                                                                                                                                                                                                rel: 517-353-0854
Fax: 517-353-9168
Email: 22313tcneibm.cl.msu.edu
Seq primer: M13 -21 dye primer.
Location/Qualifiers
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                                                                                                                                                                            Contact: Thomas Newman
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93.3%;
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                                   REFERENCE
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1890 GTGTAATTTTGCTGTACCATATAATTCTGTTT---TCATGATGACTGTAAACTGTTTATG 1946
 11.2%; Score 236; DB 12;
75.6%; Pred. No. 6.4e-35;
tive 0; Mismatches 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .799
/organism="Brassica oleracea"
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/clone="BOHKB84"
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                                                                                                                                                                                                             BH602085.1 GI:17854531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cdtown@tigr.org
DNA is from a doubled P
Seq primer: TF
Class: sheared ends.
                                                                                                                                                                                                                                                                                                                                                                                              Contact: Chris Town
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 301-838-3523
Fax: 301-838-0208
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BH602085/c
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                                                                      Brassica oleracea.
Brassica oleracea
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Wagnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 772)
Town,C.D., van Aken,S., Utterback,T. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
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                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="BoGT004"
/clone_lib="BoGT"
/clone_lib="BoGT"
/note="Vector: pH0S1, Site_l: BstXI; 2-3 kb sheared
genomic DNA inserted into pH0S1 using BstXI linkers"
187 c 176 g 210 t
BOGTO04TF BOGT Brassica oleracea genomic clone BOGTO04, DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 772;
                                                                                                                                                                                                                                                      9712 Medical Center Drive, Rockville, MD 20850, USA. Tel: 301-838-3528
Fax: 301-838-0208
Email: cdcown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn. Seq primer: TF
Class: sheared ends.
Location/Qualifiers
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Pred. No. 5e-48;
0; Mismatches 178;
                                                                                                                                                                                                                                                                                                                                                                                         /organism="Brassica oleracea"/strain="Tol000DH3"
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                                           BH525927.1 GI:17734012
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69.8%;
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BOHKB84TF BOHK Brassica oleracea genomic clone BOHKB84, DNA
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Brassica oleracea
Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Wagnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 799)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="BOHK"
/note="Vector: pHOS1; Site_l: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"
164 c 165 g 219 t
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                              232 CTACTCCTGATGAATTGAGGATGAGGCTGCTCTATCTTGAAAACAGAGGT 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Town, C.D., Van Aken, S., Utterback, T. and Fraser, C.M. Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001) Other_GSSs: BOHKB84TR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       haploid provided by Tom Osborn
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1063 ATAGGAATCCGAGGGGATATACGGTGCTTCATGTTGCTGCGATGCGGAAGGAGCCACAAT 1122
                                                                 181 TTATACTATCTCTATTGGAAAAAGGTGCAAGTTGCATCAGAAGCAACTTTGGAAGGTAGA 240
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72.2%;
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BH211724/c
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/clone="19904777"
/clone="199777"
/clone="1b="Lambda-PRI2"
/clone="1b="Lambda-PRI2"
/clone="1b="Lambda-PRI2"
/clone="190477"

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Newman, T., deBruijn, F.J., Green, P., Keegstra, K., Kende, H., McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomashow, M., Retzel, E. and Somerville, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genes galore: a summary of methods for accessing results from
large-scale partial sequencing of anonymous Arabidopsis cDNA clones
Plant Physiol. 106, 1241-1255 (1994)
                                                                                                                                                                                                                                                                                                                                                                                           T22612
4620 Lambda-PRL2 Arabidopsis thaliana cDNA clone 9905T7, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                    1947 TCTATCGTTGGC---GTCATATAGTTTCGCTCTTCGTTTTGCATCCTGTGTATT--ATTG 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        943 IGCTITIGAAAGAGGAICACACCAAICIAGAIGAIGCGIGIGCTCTICAITICGCIGIIG 1002
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463 GGGTAATATTTGATGTACCATATATATATTTTGAGTTATCATGTGTCTTAGTGTCTCTG 404
                                                                                          61 CATATTGCAATGTGAAGACCGCAACAGATCTTTTAAAACTTGATCTTNCCGATGTCAACC 120
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MSU-DOE-PRL, Michigan State University, Plant Biology Bldg.,E.
                                                                                                                                                                           2002 CIGCAGGIGIGCITCAAACAAAIGITGIAACAAITIGAACCAAIGGIAIACAGAIT 2057
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On Nov 6, 1997 this sequence version replaced gi:932513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 10; Length 258;
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/strain="var columbia"
/db_xref="taxon:3702"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 517-353-0854
Fax: 517-353-9168
Email: 22313tcn@lbm.cl.msu.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq primer: T7 dye primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Thomas Newman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T22612.1 GI:2597193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49 c
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Matches 244; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      sednence.
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DEFINITION
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                                                                                                                                                                                                                                                                                                                             RESULT 7
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SALK_006564 Arabidopsis thallana TDNA insertion lines Arabidopsis thallana genomic clone SALK_006564, DNA sequence.

BH211724
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Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Heller,C., Kim,C.J., Jeske,A., Koesema,E., Meyers,M.C., Parker,H., Prednis,L., Shinn,P., Stevenson,D.K., Zimmerman,J. and Ecker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ξ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="SALK_006564"
/clone="SALK_006564"
/clone=lib="Arabidopsis thaliana TDNA insertion lines"
/note="PGFR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   972 GATGATGCGTGTGTCTTCATTTCGCTGTTGCATATTGCAATGTGAAGACCGCAACAGAT 1031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1032 CTTTTAAAACTIGAICTTGCCGAIGTCAACCATAGGAATCCGAGGGGATATACGGTGCTT 1091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This is single pass sequence recovered from the left border of TDNA. This sequence lies within an intron of At4926120.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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Pred. No. 1.6e-33;
0; Mismatches 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
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us-08-908-884-2.rst

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buse249 614 bp mRNA linear EST 20-MAR-2001
EM1_71_bl2.bl_A002 Embryo 1 (EM1) Sorghum bicolor cDNA, mRNA
sequence.
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1 (bases 1 to 614)

1 (bases 1 to 614)

An Est database from Sorghum: developing embryos

Unpublished (2000)
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                                         1707 CTACAAAAGAAGCAAAGGTACATGGAAATACAAGAGACACTAAAGAAGGCCTTTAGTGAG 1766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1587 AAAACCGTGGAACTCGGGAAACGATTCTTCCCGCGCTGTTCGGCAGTGCTCGACCAGATT 1646
                                                                                                                                                                                                                                                                                           1467 TTCATAGTGACTAGCCTCGAGCCTGACCGTCTCACTGGTACGAAGAGAACATCACCGGGT 1526
                                                                                                                                                                                                                                                                                                                                                                               1527 GTAAAGATAGCACCTTTCAGAATCCTAGAAGAGCATCAAAGTAGACTAAAAGCGCTTTCT 1586
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            612 GAGCAAGCAGAAAGAAGAAGAAGAAGACTTCATTATCTCTTGCTATGGCA 553
                                                                                                                                                                                                                                                  492 CTTTTTCCCATGGAAGCAAAGTTGCAATGGACATTGCTCAAGTTGATGGCACGTCTGAA 433
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    Gaps
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                                                                                                                                                                                                                                                                                                                    1407 CTTTTTCCAACGGAAGCACAAGCTGCAATGGAGATCGCCGAAATGAAGGGAACATGTGAG
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Department of Botany
The University of Georgia
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
Plant: 706 542 1805
Fax: 706 542 1805
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Э
  Indels
  Mismatches 192;
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/db_xref="taxon:4558"
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High quality sequence stop: 610
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    Conservative
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BG464249.1
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    341;
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    Matches
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KEYWORDS
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XhoI; Leaves of various stages were shaken in liquid
nitrogen, shearing off trichomes. This procedure yielded a
mixture of cells highly enriched for trichomes, with minor
contamination by other types of leaf cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST 18-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eŭkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lycopersicon.

1 (bases 1 to 613)

1 (bases 1 to 613)

Lidang, J., Vrebalov, J., White, R., Matern, A.L., Lakey, J., Holt, I.E. Liang, F., Hansen, T.S., Upton, J., Ronning, C.M., Craven, M.B., Fujii (C.Y., Bowman, C.L., Nierman, W., Fraser, C.M., Venter, J.C., Martin, G.B., Tanksley, S.D. and Glovannoni, J.
Generation of ESTs from wild tomato (Lycopersicon pennellii)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST290093 L. pennellii trichome, Cornell University Lycopersicon bennellii cDNA clone cLPT119 similar to A. thallana transcription factor inhibitor I kappa B homolog, mRNA sequence.
                                                                                                                                                                                                                                                      TGTGTAGAAATACTAGAGCAAGAAGACAAACGAGAACAAAT---TCCTAGAGATGTTCCT 1328
                                                                                                                                                                                                                                                                                                                                        CCCTCTTTTGCAGTGGCGGCCGATGAATTGAAGATGACGCTGCTCGATCTTGAAAATAGA 1388
                                                                                                                                                                  ATGCCGGTTGAATGTAATATATCCCGGAGCAATGCAAGCATTCTCTCAAAGGCCGACTA 1271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="L. pennellii trichome, Cornell University"
//tissue_type="trichome"
/dev_stage="mixed stages"
/lab_host="SOLR"
                                                                                                                                                                                               223 AAAGCGGATGACTACAAAACTAGTACGAGGACGGTACGCTTCTCTGAAAGGCGGATA 164
                        CATGTTGCTGCGATGCGGAAGGAGCCACAATTGATACTATCTCTATTGGAAAAAGGTGCA
                                                                                                       1152 AGTGCATCAGAAGCAACTTTGGAAGGTAGAACCGCACTCATGATCGCAAAACAAGCCACT
                                                                                                                                                                                                                                                                                                                                                              103 CTTTCTCTTCCAGTAACTCCAGAGGAGTTGAGGATGAGGTTGCTCTATTATGAAAACCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 613;
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/db_xref="taxon:28526"
/clone="cLPT119"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 212.8; DB 9
Pred. No. 1.7e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lycopersicon pennellii.
Lycopersicon pennellii
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 prime sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .613
                                                                                                                                                                                                                                                                                                                                                                                                                       GITGCACTTGCT 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGTATGCTTTCT 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: CUGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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KEYWORDS
SOURCE
ORGANISM
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ORIGIN
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                                                                                                                                                                  1212
                                                                                                                                                                                                                                                    1272
                                                                                                                                                                                                                                                                                                                                     1329 (
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AUTHORS
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us-08-908-884-2.rst

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/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; supplier: Cornell University, Tanksley lab; sequencing; The Institute for Genomic Research. Roots well isolated from in vitro grown stem cuttings on CM medium. Roots were isolated two weeks after placing the stem cuttings from in vitro grown plants on medium."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            961 ACACCAATCTAGATGATGCGTGTGCTCTTCATTTCGCTGTTGCATATTGCAATGTGAAGA 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1081 ATACGGTGCTTCATGTTGCTGCGATGCGGAAGGAGCCACAATTGATACTATCTGTATTGG 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .261 AAGGCCGACTATGTGTAGAAATACTAGAGCAAGAAGACAAACGAGAACAAATTCCTAGAG 1320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1021 CCGCAACAGATCTTTTAAAACTTGATCTTGCCGATGTCAACCATAGGAATCCGAGGGGAT 1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1141 AAAAAGTGCAAGTGCATCAGAAGCAACTTTGGAAGGTAGAACCGCACTCATGATCGCAA 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AACAAGCCACTATGGCGGTTGAATGTAATAATATCCCGGAGCAATGCAAGCATTCTCTCT 1260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGITACTGAGGTTCTTGGACTGGGTGTTGCTAATGTCAACCTTCGGAATACACGTGGTT 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 426 CTAAGGGAGCTCATGCATCAGAAATTACATTGGATGGGCAGAGTGCTGTTGGCATCTGTA 485
 Utterback, T., Chiemingo, A., Bougri, O., Buell, C.R., Ronning, C., Tanksley, S. and Baker, B.
Generation of ESTs from potato roots
Unpublished (2001)
Contact: Research Genetics, Libraries Division
Tel: 1-800-711-6195
Email: cdna@fessgen.com
Division tel 1-800-711-6195, email cdna@fessgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       186 TATACAAGGCATTGGATTCAGATGATGTTGAACTTGTCAAGCTTCTACTTAATGAGTCTG 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 901 TACATAAGGCACTTGACTCGGATGATATTGAGTTAGTCAAGTTGCTTTTGAAAGAGGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1321 ATGTTCCTCCTCTTTTGCAGTGGCGGCCGATGAATTGAAGATGACGCTGCTCGATCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    606 ATGCATTATTTTCTTCCCCCATGTTGGCCGATGATCTGCCCATGAAACTGCTCTACCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGAGGCTGAGTAGGCCTAAGGAGTACCATGCAAAAACAGAACAAGGCCAGGAAGCAAACA
                                                                                                                                                                                                               1. 700
/organism="Solanum tuberosum"
/organism="Rennebec"
/du_xref="taxon:4113"
/clone="cpRollOG3"
/clone=lib="potato roots"
/tissue_type="roots"
/dev_stage="in vitro grown stem cuttings"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 187.8; DB 10;
Pred. No. 8.9e-26;
0; Mismatches 197;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             654 bp
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1. .700
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                                                                                                                                                                          primer: T3.
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Best Local Simil
Matches 306; C
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                                           TITLE
JOURNAL
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BG124935
LOCUS
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                                                                              COMMENT
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/clone_lib="Embryo 1 (EM1)"
//note="Organ: Embryos germinated for 24 hr; Vector:
pBluescript II from Lambda Zap II; Site_l: XhoI; Site_2:
ECORI; The library was made from poly-A RNA in the cloning
vector lambda ZAP II. Clones to be sequenced were
                                                                                                                                                                                                             ij
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1 (bases 1 to 700)
van der Hoeven, R., Sun, H., Karamycheva, S.A., Tsai, J., Van Aken, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGTGTAGAAATACTAGAGCAAGAAGAGAACAGAGAACAATTCCTAGAGATGTTCCTCCC 1331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1152 AGTGCATCAGAAGCAACTTTGGAAGGTAGAACCGCACTCATGATCGCAAAACAAGCCACT 1211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCTTTTGCAGTGGCGGCCGATGAATTGAAGATGACGCTGCTCGATCTTGAAAATAGAGTT 1391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          972 GATGATGCGTGTGCTCTTCATTTCGCTGTTGCATATTGCAATGTGAAGACCGCAACAGAT 1031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1032 CTTTTAAAACTTGATCTTGCCGATGTCAACCATAGGAATCCGAGGGGATATACGGTGCTT 1091
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                                                                                                                                                                                                                                                                                                                                                                                                                     428 AATCATGGGGATTACTTTGGGCCTACTGAGGATGGAAAGCCTTCTCCTAAAGATAAGATAA 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         804 GAAAAGTCATTGCCGGAAGAGCTTGTTAAAGAGATAATTGATAGACGTAAAGAGCTTGGT 863
                                                                                                                                                                                                                                                                                                                           ---AAACATGTCTCGAATGTACATAAGGCA 911
                                                                                                                                                                                                                                                                                                                                                             68 TTAGTITTACCAGAGGACAAGGGCTTCCCTAACATACATGTAAGAAGAGTACACAGGGCG 127
                                                                                                                                                                                                                                                                                                                                                                                                912 CTTGACTCGGATGATATTGAGTTAGTCAAGTTGCTTTTTGAAAGAGGATCACCAATCTA 971
                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                    488 TGTATTGAGATACTAGAGCAAGCTGAAAGAAGGACCCACATCTTGGAGAAGCATCAGTT
                                                                                                                                                                                                             12;
                                                                                                                                                                          DB 10; Length 614;
                                                                                                                                                                                                             Indels
                                                                                                                                                                      10.0%; Score 211.4; DB 10;
llarity 60.8%; Pred. No. 3.1e-30;
Conservative 0; Mismatches 226;
                                                                                              prepared by mass excision."
125 c 146 g 155 t
                                                                                                                                                                                                                                                                                                                         TTGGAGGTACCTAAAGTAAAG-----
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Solanum tuberosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNA sequence.
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Length 700;

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                                                                                  DEFINITION
                                                                                                                                                                                  ORGANISM
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TITLE
JOURNAL
COMMENT
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BG598808
                                                                                                                ACCESSION
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KEYWORDS
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                                   RESULT 13
BH602094
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EST470581 tomato shoot/meristem Lycopersicon esculentum cDNA clone cTOF7K1 5' sequence, mRNA sequence.
BG124935
                                                                                              Lycopersicon esculentum
Sukaryota, Viiidiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Asteridae, euasterids I; Solanales, Solanaceae, Solanum,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /hote-weetor: pBluescript SK(-); Site_1: EcoR1; Site_2: Xhol: Small expanding leaves from the growing tip were taken from greenhouse plants (4-6wks old TA496). Tissue was immediately frozen in liquid nitrogen."
                                                                                                                                                                      l (bases I to 654)
van der Hoeven, R., Bezzerides, J., Sun, H., Cho, J., Utterback, T.,
Hansen, C., Ronning, C. and Tanksley, S.
Generation of ESTs from tomato shoot/meristem tissue
Contact: CUGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1353 GAATTGAAGATGACGCTGCTCGATCTTGAAAATAGAGTTGCACTTGCTCAACGTCTTTTT 1412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1473 GTGACTAGCCTCGAGCCTGACCGTCTCACTGGTACGAAGAACATCACCGGGTGTAAAG 1532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1533 ATAGCACCTTTCAGAATCCTAGAAGAGCATCAAAGGTAGACTAAAAAGCGCTTTCTAAAACC 1592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGTGAGGACTTGACTCAACTGGCTTGCGGAGAAGACGACACTGCTGAGAACGACTACAA 1712
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                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="crOF7K1"
/clone_lib="tomato shoot/meristem"
/tissue_type="shoot/meristem"
/dev_stage="developing shoots from 4-6wks old plants"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 CTGGCTAGCAT---GAGGAAGAAGAAGATAGCTGATGCACAGAGGACAACAGTGGATTTGAAC 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                299 GCTGATGACTTGTCTGAGATAGCTTACATGGGGAACGATACAGTAGATGAGTCTCAACTG 358
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                                                                                                                                                                                                                                                                                          Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 1.4e-25;
0; Mismatches 167; Indels
                                                                                                                                                                                                                                                                                                                                                      /organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
                                                                                                                                                                                                                                                                              Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 186.8;
                                                BG124935.1 GI:12625123
EST.
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Matches 300; Conservative
                                                                                                                                                               Lycopersicon
                                                                                  tomato
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ORGANISM
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AUTHORS
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COMMENT
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                               ACCESSION
                                                VERSION
KEYWORDS
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BG598808 65T Solanum tuberosum cDNA clone cSTS22E2 5' sequence, mRNA sequence.
BG598808 1 GI:13618649
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GSS 15-DEC-2001
                                                                                                                                                                               Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          621 TICAAGATCCCTGAATTAATTACTCTCTATCAGAGGCACTTATTGGACGTTGTAGACAAA 680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              681 GTTGTTATAGAGGACACATTGGTTATACTCAAGCTTGCTAATATATGTGGTAAAGCTTGT 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   741 ATGAAGCTATTGGATAGATGTAAAGAGATTATTGTCAAGTCTAATGTAGATATGGTTAGT 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           801 CTTGAAAAGTCATTGCCGGAAGAGCTTGTTAAAGAGATAATTGATAGACGTAAAGAGCTT 860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="BOHK"
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared genomic DNA inserted into pHOS1 using BstXI linkers" 133 c 183 g 252 t
                                                                                                                                                    Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheol
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
I (bases 1 to 785)
Town.C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
Other_GSSS: BOHKB84TF
                    BOHK Brassica oleracea genomic clone BOHKB84, DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            haploid provided by Tom Osborn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGTTTGGAGGTACCTAAAGTAAAGAAACATGTCTCGAATGTACATAAGG 909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 172.2; DB 12; Length
Pred. No. 7.9e-23;
); Mismatches 73; Indels
  linear
                                                                                                                                                                                                                                                                                                                                                                                                    9712 Medical Center Drive, Rockville, MD
  DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
1. 785
/organism="Brassica oleracea"
  785 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:3712"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="TO1000DH3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.2%; Scur
74.7%; Pred
0; }
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="BOHKB84"
                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled ha
Seq primer: TR
Class: sheared ends.
                                                                                     BH602094.1 GI:17854540
                                                                                                                                                                                                                                                                                                                                                           Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 74.73
Matches 216; Conservative
                                                                                                                                   Brassica oleracea
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496 ITTATITGAAAATAGAGTGGCATTGGCACGGATGTTATITCCTCAGGAAGCCATGCTAGC 555
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800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
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Pred. No. 1.4e-20;
0; Mismatches 149;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ų
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Location/Qualifiers
                                                                                                                                                                                                                                                   455 bp
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/db_xref="taxon:4568"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98 g
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                                                                                                                                                                                                                                                                                                                                                               BE493178.1 GI:9659771
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                                                           1433 AATGGAGATCGC 1444
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                                                                                             |||||| || ||
556 TATGGAAATAGC 567
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Best Local (
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ORIGIN
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BE493178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pBluescript SK(-); Site_1: BCORI; Site_2: XhoI; Various sizes of sprouting eyes (2mm to 15mm) were taken from tubers: The tubers were incubated at 26C in the dark for 2-3 weeks prior to sprouting. The eyes were frozen in liquid nitrogen immediately upon removal from tubers."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                       Tracheophyta;
                                             Spermatophyta; Magnoliophyta; Embryophyta; Tracheophy Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterida! Solanales; Solanaceae; Solanum.

1 (bases 1 to 667)

2 (bases 1 to 667)

3 (bases 1 to 667)

4 (bases 1 to 667)

5 (bases 1 to 667)

6 (bases 1 to 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     956 GGATCACACCAATCTAGATGATGCGTGTGCTCTTCATTTCGCTGTTGCATATTGCAATGT 1015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1016 GAAGACCGCAACAGATCTTTAAAACTTGATCT---TGCCGATGTCAACCATAGGAATCC 1072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1073 GAGGGGATATACGGTGCTTCATGTTGCTGCGATGCGGAAGGAGCCACAATTGATACTATC 1132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1133 TCTATTGGAAAAAGGTGCAAGTGCATCAGAAGCAACTTTGGAAGGTAGAACCGCACTCAT 1192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1193 GATCGCAAAACAAGCCACTATGGCGGTTGAATGTAATAATATCCCGGAGCAATGCAAGCA 1252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1253 TTCTCTCAAAGGCCGACTATGTGTAGAAATACTAGAGCAAGAAGACAAAACGAGAACAAAT 1312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1313 TCCTAGAGATGTTCCTCCTCTTTTGCAGTGGCGGCCGATGAATTGAAGATGACGTGCT 1372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1373 CGAICTIGAAAATAGAGTIGCACTIGCICAACGICTITITICCAACGGAAGCACAAGCIGC 1432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               896 GAATGTACATAAGGCACTTGACTCGGATGATATTGAGTTAGTCAAGTTGCTTTTGAAAGA 955
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   256 ACTACTTGCAAAAGGAGCATCGGTCTTGGATACTACACGCGACGACATACAGCACTATC 315
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The Institute for Genomic Research
For clone info: please contact Research Genetics, Libraries
Division tell 1-800-711-6195, email cdna@resgen.com
Seq primer: M13F-R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Solanum tuberosum"
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/clone="cSTS2RE"
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/dev_stage="12-14 weeks post harvest"
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0; Mismatches 233;
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ENKATYCHA, VITIGIDALATE, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Vitidiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Trittceae; Tri
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/dab_host="E. coli XLOLR"
/note="Vector: Lambda pBk-CMV (Lambda Zap Express),
excised phagemid; Site_1: ECORI; Site_2: XhoI; The tissue,
total RNA, and poly(A) RNA were prepared, a cDNA library
was made, and the CDNA clones were in vivo excised at the
University of California, Davis (V. Echenique, B. Stamova
J. Dubcovsky). Plasmid DNA preparations and DNA
sequencing were performed in the OD Anderson lab (all
BE493178 455 bp mRNA linear EST 16-APR-2001
WHE0570_C11_F22ZE Triticum monococcum vegetative apex cDNA library
Triticum monococcum cDNA clone WHE0570_C11_F22, mRNA sequence.
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/clone_lib="Triticum monococcum vegetative apex cDNA
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Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: Stratagene T3 primer.
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142 AAATTATTGATTCACGGATAACTCTTGGATTAGCTTCACCCGAAGACAATGGCTGTCCTA 201

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     GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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0; Mismatches 546;
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/strain="ecotype Columbia"
/db_xref="taxon:3702"
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                DDIELVKLLLKEDHTNLDDACALHFAVAYCNVKTATDLLKLDLADVNHRNPRGYTVLH
VAAMRKEPQLILSLLEKGASASEATLEGRTALMIAKQATMAVECNNIPEQCKHSLKGR
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                                                                                                                                                                                                                                                                              Score 578.4; DB 8 Pred. No. 3.7e-138
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62.8%;
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Koesema,E., Chen,H., Cheuk,R., Kim,C.J., Meyers,M.C., Shinn,P.,
Banh,J., Bowser,L., Carrinci,P., Dale,J.M., Goldsmith,A.D.,
Hayashizaki,Y., Ishida,J., Jiang,P.X., Jones,T., Kamiya,A.,
Karlin-Neumann,G., Kawai,J., Lam,B., Lee,J.M., Lin,J., Liu,S.X.,
Miranda,M., Narusaka,M., Nguyen,M., Onodera,C.S., Palm,C.J.,
Pham,P.K., Quach,H.L., Sakurai,T., Satcul,M., Scuthwick,A.,
Tang,C.C., Toriumi,M., Yamada,K., Yamada,K., Yu,G., Yu,S.,
Shinozaki,K., Davis,R.W., Theologis,A. and Ecker,J.R.
Direct Submission

L Submitted (08-AuG-2001) Salk Institute Genomic Analysis Laboratory
(SIGnAL), Plant Biology Laboratory, The Salk Institute for
Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
                                                                                                                                                                                                    Eukaryota; Viridipantae; Streptophyta; Embryophyta; Tracheophyta; Bukaryota; Viridipantae; Streptophyta; Eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

E (bases 1 to 2154)

S Koesema,E., Chen,H., Cheuk,R., Kim,C.J., Meyers,M.C., Shinn,P., Banh,J., Bowser,L., Carninci,P., Dale,J.M., Goldsmith,A.D., Hayashizaki,Y., Ishida,J., Jiang,P.X., Jones,T., Kantlin,A.D., Miranda,M., Narusaka,M., Nauyen,M., Codera,C.S., Palm,C.J., Pham,P.K., Quach,H.L., Sakurai,T., Satou,M., Seki,M., Southwick,A., Shinozaki,K., Davis,R.W., Theologis,A. and Ecker,J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL CDNAS: Koesema, E., Chen, H., Cheuk, R., Kim, C.J., Meyers, M.C., Shinn, P., Banh, J. Bowser, L., Dale, J.M., Goldsmith, A.D., Jiang, P.X., Jones, T., Karlin-Neumann, G., Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M., Nguyen, M., Onodera, C.S., Pallm, C.J., Paham, P.K., Quach, H.L., Southwick, A., Tang, C.C., Toriumi, M., Yamada, K., Yamanura, Y., Yu, G., Yu, S., Davis, R.W., Theologis, A., and Ecker, J.R.
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ALQLLSNSFESYFDSPDDFYSDAKLVLSDGFBSYSFHRCVLSARSSFFKSALAAAKKEK
DSNNTAAVKLELKEIAKDFYSTGYFDSVYVTVALYVY SSRVKPPPRGVSECADBNCCHVAC
RPAVDPMLEVLYLLAFFKIPELITLYORHLLDVVDKVVIEDTLVILKLANICGKACM
LLDRCKEIIVKSNVDMVSLEKSLPEELVKEIIDRRKELGLEVPKVKKHVSNVHKALDS
                                PLN 20-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     collection and clustering of RAFL cDNAs (RAFL CDNA : 'RIKEN Arabidopsis Full-Length cDNA') : Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RIKEN Genomic Sciences Center (GSC) members carried out the
                   AIUSU455 2154 bp mRNA linear PLN 20
Arabidopsis thaliana At1g64280/F15H21_6 mRNA, complete cds
AY050455
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/db_xref="taxon:3702"
/chromosome="1"
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/db_xref="GI:15215850"
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COMMENT

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GGCTTGTGGGATTTCAGTAAGTCTCCGGAGGAAGGAAAATCTGCTTCGAATGATCGGTTAT 1416 GCATTGAGATTCTGGAGCAAAGAAGAAGAGACCCTCTGCTAGGAGAAGCTTCTGTAT 1476 TTCTAGATCTTGCACTTGCTGATATTAATCATCAAAATTCAAGGGGATACACGGTGCTGC 1236 GIGCATCAGAAGCAACTIIGGAAGGIAGAACCGCACTCAIGAICGCAAAACAAGCCACTA 1162 TGGATTCTGATGATGTTGAATTACTACAAATGTTGCTAAGAGGGGGCATACTACCTAG 1116 997 TACAAGGGCCTGAAAGCAACGGTTTTCCTGATAAACATGTTAAGAGGATACATAGGGCAT 1056 876 936 ATAAAGCCTTGCCTCATGACATTGTAAAACAAATTACTGATTCACGAGCGGAACTTGGTC 996 816 694 576 969 514 574 634 534 GACCTTCTGATCTGACATCGATGGAAGAAAGCACTTCAAATCGCCAAGAGGCTCACTA GTAAAGTTAGGCCTTCACCTAAAGATGTGTGTGTTTGTGTGGACAATGACTGCTCTATG TGGCTTGTAGGCCAGCTGTGGCATTCCTGGTTGAGGTTTTGTACACATCATTAACCTTTC AGATCTCTGAATTGGTTGACAAGTTTCAGAGACACCTACTGGATATTCTTGACAAAACTG CAGCAGACGATGTAATGATGGTTTTATCTGTTGCAAACATTTGTGGTAAAGCATGCGAGA ATGATGCATATGCTCTCCATTATGCTGTAGCGTATTGCGATGCAAAGACTACAGCAGAAC ATGTTGCAGCCATGAGGAAAAGAGCCTAAAATTGTAGTGTCCCTTTTAACCAAAGGAGCTA CGGAGTTTGACTACTTCGCCGACGCTAAGCTTGTGGTTTCCGGCCCGTGTAAGGAAATTC AAAAGGAGAAAAATAGTAGT---------AAGGTGGAATTGAAGGTGA CGGTGCACCGGTGCATTTTGTCGGCGAGGAGTCCGTTCTTTAAGAATTTGTTCTGCGGTA Mismatches ; Conservative

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PAT 07-SEP-2000
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disease resistance in
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  CICTIGCTATGGCAGGCGATGATTIGCGTATGAAGCTGTTATACCTTGAAAATAGAGTTG
           GCCTGGCTAAACTCCTTTTTCCAATGGAAGCTAAAGTTGCAATGGACATTGCTCAAGTTG
                                                    ATGGCACTTCTGAGTTCCCACTGGCTAGCATCG----GCAAAAAAGATGGCTAATGCACAGA
                                                                                                                          GGACAACAGTAGATTTGAACGAGGCTCCTTTCAAGATAAAAGAGGAGCACTTGAATCGGC
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Pred. No. 9.7e-138;
0; Mismatches 547;
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Uknes,S.Joseph, Hunt,M.Denise, Steiner,H.
Altered forms of the NIMI gene conferring
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a 417 c 474 g
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Best Local Similarity 62.7%;
Matches 981; Conservative
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                                              GAATATGATAAGACTAACAACATCTCCTCATCTTGTTCCTC 1957
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                                                                                          TTCTAAATAAGATCATGGATGCTGATGACTTGTCTGAGATAGCTTACATGGGGGAATGATA 1833
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Uknes, S. Joseph, Hunt, M. Denise, Steiner, H.
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//protein_id="CAD22848.1"
//do_xref="C1:18616499"
//tanslatton="MPFSAMRHLLDFLDKVEVDNLPLILSVANLCNKSCVKLFERCM
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VELVRMLLTGGGTNLDDAFALHYAVEHCDSKITTFELLDIALADVNLRNPRGYTVLHIA
KRRDPRIVYSELTRGARPSDFTFDGRRAVOISKRITKHGHOFYFGNTERGERSPNOKLC
IEILEQABREDPQLGSALSLALAGDCLRGKLLYLENRVALARIMFPIEARVAMDIAQ
VDGTLEFTLGSSTNPPLEITTVDLNDTSFKMKEEHLARMRALSKTVELGKRFPRCSN
VMCTLEFTLGSSTNPPLEITTVDLNDTSFKMKEEHLARMRALSKTVELGKRFPRRCSN
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VMCTLEFTLGSSTNPTLTTVSSCSSTST
    06-FEB-2002
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                                                                                                     Eukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
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                                                                                                                                                             Wang, H.X., Salmeron, J.M., Willits, M.G. and Lawton, K.A. Monocotyledonous plant genes and uses thereof Patent: WO 0166755-A 19 13-SEP-2001; Syngenta Participations AG (CH)
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larity 67.0%; Pred. No. 4.7e-125;
Conservative 0; Mismatches 374;
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/note="unnamed protein product"
   DNA
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/db_xref="taxon:4565"
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Uknes,S.Joseph., Hunt,M.Denise., Steiner,H.-Y. and Ryals,J.Andrew.
Altered forms of the NIMl gene conferring disease resistance in
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CTAAAAATCGTTGTCTCCCTTTTAACCAAAGGTGCCCGGCCTTCAGATTTTACATTTGATG 1006
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                                                               CTGAAGAAGGAAAGCCGTCTCCCAATGATATATGCATTGGAGATATTGGAGCTG
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                                                                                                                                                                                                      AAAGAAGACCCTCTGCTAGGAGAAGCTTCTGTATCTCTTGCTATGGCAGGCGATGATT
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                                                                                                                       TGCGTATGAAGCTGTTATACCTTGAAAATAGAGTTGGCCTGGCTAAACTCCTTTTTCCAA
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CGGTGCACCGGTGCATTTTGTCGGCGAGGAGTCCGTTCTTTAAGAATTTGTTCTGCGGTA
                                                     CTTTCCACCGGTGCGTTTTGTCACGAGAAGCTCTTTTTTCAAGAGCGCTTTAGCCGCCG
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GFPRHEHVRLDSDDVELVRMLITEGOTNLDDARALHYAVEHCDSKITTELLDLA
LADVNHRNPRGYTVLHIAARRREPKIIVSLITKGARPADVTFDGRRAVQISKRLTKQG
DYFGYTEEGRFSPFRDRLIEILEGARRRDPQLGEASVSLAMAGESLERGRLITLENRVA
LARIMFPMEARVAMDIAQVDGTLEFNLGSGANPPPERQRTTYVDLNESFIMKEEHLAR
HTALSKTVELGKRFFFRGSNVLDKINDDETDPVSLGRDTSAEKRRFHDLQDVLQKAF
HTALSKTVELGKRFFFRGSSSTSTGLGAIRRR"

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/db_xref="GI:18616495"
/translation="CaFPPARAGGLLLLLLAELINLFQRRLLDVLDKVEVDNLLLIL
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
CITITGCAGTGGCGGCCGATGAATTGAAGATGACGCTGCTCGATCTTGAAAATAGAGTTG 1342
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                                GCCTGGCTAAACTCCTTTTTCCAATGGAAGCTAAAGTTGCAATGGACATTGCTCAAGTTG
                                                     CACTTGCTCAACGTCTTTTTCCAACGGAAGCACAAGCTGCAATGGAGATCGCCGAAATGA
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                                                                                                ATGGCACTTCTGAGTTCCCACTGGCTAGCATCG---GCAAAAAAATGGCTAATGCACAGA
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Sequence 15 from Patent WO0166755.
AX351141
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/db_xref="taxon:4530"
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Db	Qy Dp	Qy Db	Oy Dp	Oy Dp	Qy	Qy Dp	Qy Db	Qy Db	Qy Db	Qy Dp	Qy Dp	Qy Db	QY Dp	Qy Db	Qy Db	Oy Db	Qy Db

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Uknes,S.Joseph, Hunt,M.Denise, Steiner,H. and Ryals,J.Andrew.
Altered forms of the NIM1 gene conferring disease resistance
                                                                                                                                                                                                                                                                                    600 GATGCTGTAATGAGTGTATTGGCTTATTTGTATAGTGGTAAAGTTAGGCCTTCACCTAAA
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                                                                                                                                                                                                                                         Length 1194;
                                                                                                                                                                                                                                     Score 490; DB 6; Length 11
Pred. No. 2.3e-115;
0; Mismatches 410; Indels
      linear
     DNA
                                                                                                                                   Plants
Patent: US 5986082-A 13 16-NOV-1999;
Location/Qualifiers
Sequence 13 from patent US 5986082.
                                                                                                                                                                                                    322
                                                                                                                                                                                    /organism="unknown"
227 c 294 g
                                     AR087506.1 GI:10014269
                                                                                                                                                                                                                                     Query Match 22.6%;
Best Local Similarity 64.5%;
Matches 771; Conservative (
                                                                                      Unclassified.
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                                                            Unknown
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           DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
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AUTHORS
TITLE
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Orga sativa genomic DNA, chromosome 1, PAC clone:P0001B06.
AP002537
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Eukaryota, Virialplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae, Oryza.
1 (bases 1 to 140304)
Sasaki, T., Matsumoto, T. and Yamamoto, K.
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
clone: P0001B06
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TTATTGTCAAGTCTAATGTTGATATCATAACCCTTGATAAAGCCTTGCCTCATGACATTG 960
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                          1141 CTGTAGCGTATTGCGATGCAAAGACTACAGCAGAACTTCTAGATCTTGCACTTGCTGATA
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                                                                                961 TAAAACAAATTACTGATTCACGAGCGGAACTTGGTCTACAAGGGCCTGAAAGCAACGGTT
                                                                                                                                                                     1021 TTCCTGATAAACATGTTAAGAGGATACATAGGGCATTGGATTCTGATGATGTTGAATTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryza sativa (cultivar:Nipponbare) DNA, clone:P0001B06.
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                                                                                                                                                                                                                                       1500 TIGCGTATGAAGCTGTTATACCTTGAAAATAGAGTTGGCCTGGCTAAACTCCTTTTTCCA
                                                                     Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trach
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooldeae; Triticeae; Triticum.
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Monocotyledonous plant genes and uses thereof
Patent: WO 0166755-A 113-SEP-2001;
Syngenta Participations AG (CH)
Location/Qualifiers
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Pred. No. 4.8e-90;
0; Mismatches 227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Triticum aestivum"
/db_xref="taxon:4565"
1396. 2163
2164. 2337
2338. 2532
2533. 2933
294. 3188
a 872 c 911 g 1355 t
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69.9%;
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Matches 528; Conservative
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(October 1998 version). The genomic sequence was searched against NVBI NonRedutant Protein database, nr (ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA sequence database at RGP. Protein homologies of the coding regions were searched against RGP. Protein homologies of the coding regions were searched against the identified cDNA sequences using BLASTN 2.0 with the corresponding DDBJ accession no. and RGP clone ID.

A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative' and 'like protein'. A gene without almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted with a gene prediction program is classified as a 'hypothetical' protein.

The orientation of the sequence is from SP6 to T7 of the PAC clone. This sequence of P0001B06 clone has an overlap with P0671B11.

DebbJ:AP002746 ) clone at the position 10 61357 of 5' end. The sequence of this clone starts at the position 107016 of P0671B11.

Detailed information on overlap and assembly quality together with annotation of this entry is available at http://rgp.dna.affrc.go.jp/GenomeSeq.html Detailed information on overlap and assembly quality together with annotation of this entry is available at http://rgp dna.affrc.go.jp/GenomeSeq.html.
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GLLHRCAIGAAHNSLCRVLLHEVWEWBGEAAAAAAAAAAAEAAEDRALRGIWAVGLLCR
WQPQPQCSSKLTISCTPLH"
7047. 7694
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AKPPGSSQAEWSVASNESLFSIHHGARPSGDLCGFYAGESRSHFDTFTYDEAMAGAAG
DHTSDWKLATVAEGSPGGSARSDATDGGGGAAKQKAAIDFRRHESGSAGSSSNFSFAF
PMYAADDAIVIGGDDDVAEEEGLRRVVPSAEEGGGAAAGGYAGVGVRGDDAGGGAAAA
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/gene="P0001B06.4"
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/gene="P0001806.4"
/note="hypothetical protein
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/note="hypothetical protein"
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join(2486. .2566,4546. .4833)
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/gene="P0001B06.2"
/note="hypothetical protein"
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/organism="Oryza sativa"
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FEATURES

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/translation-manabahaahsplrrrlphhrgrrllavaalspeppappy
Trspppprkgyprrrnbullgergigerrrlphyrgrgucgorpergerllar
Trspppprkgyprrrnbullgergigerrrnbullgerllar
Trspppprkgyprrrnbullgergigerrrnbullgerllar
VRRIRRGAPABAAAAAAAAAPADPLAADGGGCRAGSLAYAAOIRHKHLGVRE
LLVNRGKPDPRKMESSEDALLKPIVPCDEIFRYRRKMEFSFGTRRWMGREWEERD
EVVRERVPGEGLGLHAPGFFDRVLHVBRCLLGSBPADKTLIVDGTWLDPALGLT
PYDVHRHVGFLKHLMIRTGRITTGAPEVWNVFVSCYFPELLEBLVNNITTRIPBVVS
IMNNVTSVGANTSVGEBETTLDLFGFTGILLLARBAKHVGYEVVPEAIAARKNAKLNGIS
NATFVQGDLNKINETFGKFFPRPDIIISDPNRFGMHWKLIKMLLEVKAPRIVYSCNP
AGARDLDYLCHGYBEXDLEKGCYELKGYIPVDWFPHTPHIECICVLELC"

join (19026. 19092, 19440. 19762)

join (19026. 19092. 19440. 19762)
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join(22508. .22615,22741. .22836,22932. .22994,23274. .23351,
23884. .24052,24235. .24618,25397. .25480,25581. .25726,
26248. .26508,28585. .26766,26859. .27141,28140. .28334,
28526. .28741,28826. .28978,29068. .29265)
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                                                                                                                                                        /translation="MSADGGDPFDSLPAAIAADVLGRVADGADIAAYCLASRAFLAAS
YACSRVHLRAAALARRRSVALAGGGGGGGPPGGSAIRAAAGNAASLLGPHLRSLELDAS
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                                                                                                                                                                                                                                                                                                                                                            VRLEIKCVRPDMITLDTPSMFTIKLTVÜKLGPNYQADGIVSLKNIRIESIDLKSTLIN
FABNHJITTLEIELPTSTNKYELFBAVKPEYLLÖLFAGISEVKLAPRESCEMTHCLAN
STSNGFRSCLRRLIFHLPPLKFUVPHLAPLFNNCAPSCEVTILFHADSSDDIRQAATSV
WTLRPFGIRWOWGTWN"
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VEKGEDDGSGRSTCSPCAAYVSRCGLERTVLAAVQIRQLSEGSMLRRRRKRPGDWPLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAMVAKEGNDLTEYQRLTNLFSPDEMLVLDVLESLYTVPSKISEFKINIPSGTIGRDD
SALSHRREECPSVKRSKQGKQVGECSASKTRNKRRKKLIAEEPYTEGYTSNHLDLPER
RQVDATECALNSDLERGTVDLPESTANISTKIPDLPSQLKPEINMSRRSKRKSRSPCG
SKYVVCNGADNLQAFRLÜHCLSSESLKRWCTYEWFYSAVDYPMFMDNEFVNYLNFANI.
SHLSRLTRSEWSTIRSSLGKPRRFSDHFLAAEKDKLENYRKVRQYYALLSEDSWDSL
                                                                                                                                                                                                                                                                               KAEALPSIWSTLVWSQIETSAIHAGHSLLKLRLKNAWLSVDGLKIMPNLTHLTLEFIR
                                                                                                                                                                                                                                                                                                                          LDDEDLNKLNECFPCLQILNLIGVGGLKDPKIHLHQLKTCHWEVSNVPRSLTIRAPNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(join(14597. .14704,14802. .14932,15057. .15233,
13388. .15503,15664. .15819,16008. .16116,16591. .16700,
17245. .17430,15515. .18105))
/gene="P0001B06:5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (join (14597, .14704,14802, .14932,15057, .15223, 15388, .15503,15664, .15819,16008, .16116,16591, .16700, /1745, .17440,17515, .18105))
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GFVALVTGHHNVSDESKSHKGSDQTVRASGKVRKREATGQKEKEAPHAHRSYHERRTS
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GATNNELECSSHGSPGISESAKFVQGQTFLEAKGTGSLKKRRIEQSMEQGGTIKDEHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPDLARPFSIGQQVIVRHPSTRELCDGKVVMMEQDRYNVQFDRPDLGVDEVKDTDCMP
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to Arabidopsis thaliana chromosome 4, AT4g29420"
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23884. .24052,24235. .24618,25397. .25480,25581. .25726,
26248. .26508,26585. .26766,26859. .27141,28140. .28334,
28526. .28741,28826. .28978,29068. .29265)
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similar to Arabidopsis thaliana chromosome 3, F22F7.18"
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/codon_start=1
                                                                            /protein_id="BAB16851.1"
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/db_xref="G1:10934075"
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/db_xref="G1:10934076"
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Oryza sativa
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AP002746/c
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TITLE
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SOURCE
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STYTPAPTMENDRKSLEAGTHBVLLLKQLLDLADREHKVAYSRSKRANDSSSSVSSM
STVSSSSTIEISASSGGASPEPGLSSKRRLLPWRRKSRDPDKRSSESLSQELPMKV
MDDDLAGSWETREFTSRDSETKLRTPVFFASIDQRDDSAGGESACTALVAVLAAALHA
NHPTWPTREFEBLDALIRQCSSEWRRLLODDEAHWAAFPRNHFEDLETVLAARRPTAVQHD
RAFVQFFQPDSFASISGAMSPDINKEIAAAAGGEBGRADYYIVSWNDHFFVLKVBGD
CYHVVDTLGERLEGGCDKAYMLRFDATSEMRSVSPPPSSPSPEBEVIVTGKECCREFI
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                                                                                                                                                                                                                                                                    /traislation="MMRVATYGDLPLGPTRAGAHREAEAAARPARVVVVVVRPRDTAS
SAARGESSTRVIDBSIVCEYVEGVORWERRASPAAAAGERREGGVRYGPTRLEGMP
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MSLAQAKQMVDEAMKEISENGKSSLEETGISNEATDCTGPEPESAANSELPRNLÍFNC
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                                                                          .30866,30967. .31395,31505. .31699,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54861 TTAATCATAGAAACCCAAGAGGTTATACTGTTCTTCACATTGCTGCGAGGCGAAGAGG 54802
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTGTAGCGTATTGCGATGCAAAGACTACAGCAGAACTTCTAGATCTTGCACTTGCTGATA 1200
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                                                                                                                                                                              /note="contains ESTs AU098333(E40118),AU098332(E40118)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TATCTGTTGCAAACATTTGTGGTAAAGCATGCGAGAGATTGCTTTCAAGCTGCATTGAGA 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTCAGAGACACCTACTGGATATTCTTGACAAAACTGCAGCAGACGATGTAATGATGGTTT 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTATTGTCAAGTCTAATGTTGATATCATAACCCTTGATAAAGCCTTGCCTCATGACATTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KRFLAAIPLREELEMERKGCADAPHRRLQIEFHFTVLKEEEDDOARR" complement(join(35488. .35671,36191. .36240))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 140304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 376.4; DB 8;
Pred. No. 4.5e-86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches 276;
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                                                                                                                                                                                                                                   /protein_id="BAB16855.1"
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                                                             LVPSASSNARLPMYM"
                                                                                                                                                                                                                      /codon_start=1
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66.3%;
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2. (bases 1 to 1083/2)

Sasaki,T., Matsumoto,T. and Yamamoto,K.

Direct Submission.

AL Submitted (0'-7101-2000) Takuji Sasaki, National Institute of
Agrobiological Resources, Rice Genome Research Program; Kannondal
2-1-2, Tsukuba, Ibaraki 305-8602, Japan
(E-mail:tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
Tel:81-298-78-741, Fax:81-298-38-7468)

On Sep 7, 2000 this sequence version replaced gi:9049479.
Genes were predicted from the integrated results of the following:
GENSCANI.0, BLASTNZ.0 as well as SplicePredictor
(October 1998 version). The genomic sequence was searched against
NCDI NonReduntant Protein database, nr
(ftp://ncbi.nlm.ni.gov/blast/db) and the cDNA sequence database at
RGP. Protein homologies of the coding regions were searched against
NCBI NonReduntant Protein database with BLASTPO.0. ESTS represent
the identified cDNA sequences using BLASTP 2.0 atthe the
corresponding DDBJ accession no. and RGP clone ID.
A gene with identity or significant homology to a protein is
significant homology to any protein name to indicate the homology (covering
almost the entire length) is classified as an 'unknown' protein. A
gene predicted with a gene prediction program is classified as a
"hypothetical' protein."

"hypothetical' protein."

"hypothetical' protein as seame prediction program is classified as a
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PAC clone:P0671B11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                  Saski,T., Matsumoto,T. and Yamamoto,K.
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
clone:P0671B11
                                                                                      1441 AAAGAAGAGCCCTCTGCTAGGAGAAGCTTCTGTATCTCTTGCTATGGCAGGCGATGATT
                                                                                                                                 TGCGTATGAAGCTGTTATACCTTGAAAATAGAGTTGGCCTGGCTAAACTCCTTTTTCCAA
CCGAAGAAGGAAAACCTTCTCCAAAAGATAGGTTATGTATTGAAATACTGGAGCAAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryza sativa (cultivar:Nipponbare) DNA, clone:P0671B11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Published Only in DataBase (2000) In press 2 (bases 1 to 168372)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54501 TCATAATGCTGGTTTCTTTGGAATTAACTGTTTTTGGT 54464
                                                                                                                                                                                                                                                                                                                                                                                                                           1561 TGGAAGCTAAAGTTGCAATGGACATTGCTCAAGTTGAT 1598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            168372 bp DNA Oryza sativa genomic DNA, chromosome 1, AP002746
AP002746.2 GI:9988419
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/cultivar="Nipponbare"
/db_xref="taxon:4530"
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24246. .24483.24832. .21823,23060. .23299,23892. .23912,
24246. .24483.24832. .24987,27438. .27609,27873. .28087)
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SALVILEAKTLDDMQIPRSELKPSNAPPHGYIPGLSAPPLGQITLPVTFGTRENFRTEN
ISFEVADFETAYHAILGRPALAKFMAVPHYTYMMMKMPGPRGVLSLRSDIKQAVTCDK
ESCDMAGTRETASAREDIRLAAATASEGEVPATKTSKSGESEAKTNKIPLDPSNPTKT
AVIGAELDCK"
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NNSGPSVLDATEIFDKLRVAPDVYFKNIKKAGSMGASTALAMTKSLYPRIEIDAIDGF
ADRTSVEAALDLISNAQNAADKIASDVVDQFRNTDLQPSSNNSDDERTDSD"
                                                                                                                                                                                                                                                                        /protein_id="BAB12689.1"
/db_xref="G1:9988423"
/translation="MYHVILARYRMILTRVGAPRHAQSPPAAVPCRRGWRRQGQRTGA
                                                                                                                                                                                                                                                                                                                                                                                                  ATAAVAGDRRGGGGGGGGGGRTPRRRRRRTNHQFTVVVNRVITKSKCDLILVMAGND
LSFAETKKKKRRNLVCPHEEARGQQTDGPDVDTSEGASSLDRMIAGGVRVSWYSLRFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="putative gypsy-type retrotransposon RIRE2 orf5"
/protein_id="BAB12691.1"
/db_xref="GI:9988425"
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/product="putative gypsy-type retrotransposon RIRE2 orf4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pseudogene, gypsy-type retrotransposon RIRE2 GAG-POL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="putative gypsy-type retrotransposon RIRE2 GAG-POL precursor"
                                                                                                                                                           /note="contains EST AU058063(E20266)
unknown protein"
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/gene="P0671B11.7"
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/codon et---/
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/gene="P0671B11.7"
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/gene="P0671B11.8"
complement(39556. .40305)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="BAB12690.1"
/db_xref="G1:9988424"
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/gene="P0671B11.6"
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NDVKRWNTNEKRRAAAAACTELELPAPPLAATHTSPSSSLLLLEPLAVPTVKTE
NTODFLQQLLPTRATBARDARAPPLAATHTSPSSSLLLLEPLANPTVVVGG
GGGGGLFPEFCMSSDDLAGAATBARDPRADGAATDGGSTSASAASGSGNWSADTGVVVVGG
GGGGGLFPEFCMSSDDLAGAATAEDDPFIGGGTYPLDPSLSSSLV*
10.017(21560. .21603.21647. .21823.23060. .23299.23892. .23912,
24246. .24483.24832. .24987,27438. .27609,27873. .28087)
// Gene="P0671b11.4"
                                                                                                                                                       .6919,
.8231,
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complement(join(17576..18104,18181..18310,18411..18546))
/gene="Roof1811.3"

complement(join(17576..18104,18181..18310,18411..18546))
/gene="Po6671811.3"

/note="contains ESTs AU082307(E0784),"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /traislation="many"

//traislation="many"

HRETNLVLISIMPSGDEAGREEGVVVIVSGGRGGRRRRHCVSEVGOPSAGSPLSSPPL

VENDITALIVGVRRGVYAPGRREAGAEPLVLALGLSVTVVPAAACCECASGNDADSPRR

PTVPENTPLOLGVYRGVYAPGRREAGAEPLVLALGLSVTVVPAAACCECASGNDADSPRR

PTVPENTPQVSGLIPWYGGLIPRYBPVSWVPSIRYRSIPNWYGSAAPPRRRRRMEA

VGVAPAPAGVPGKKLLEVKESKAAPAAPSTSWAAKRAKKLVGGDAGYVLEDVPHI

TDYLPELPTYPNPLQDNPASSVVKIPLEPRSPTAGTKRLFELHTTGAPSSSCRQYFVN

TDYTPGRIPTYPNFLGDNPASSVWKIPLEPRSPTAGTKRLFELHTTGAPSSSCRQYFVN

TDYTPGRIPTYPNFLGDGEGGYKGFYSRTVALIPRSVNDITHRGGTVLGTSRGGHDTGR

VGGLYDMYGVTSVGTGGGTGGGSKCFSRTVALIPRSVNDITHRGGTVLGTSRGGHDTGR

IVDSIKDRGINQVYIIGGDGTQKGSVVIPQEVRRGIKCSVVGVPKTIDNDIQVIDKS

FGETAFREAGRAINAAHVERSESAENIGTVKRGRRSCLIP
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GATGFTVAPVAPVGRHAXIPFRITLEGROKVVTTDFMARRVLCSTNQPCFLSHEDVEHL
KHDDDEHHLHNTQLLEGESSPVKNOSSKCNGTAAPV
complement(join(9764..9865,9991..10063,10383..10500,
10566..10682,10803..10898,10989..11084,11181..11324,
11330..12440,12703..12752,13035..13225,13247..13431,
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/protein_id="pAB12687.1"
/db_xref="G1:9988421"
/translation="MLISEYWWNATYKFDMFSTHEHEALOKREPIKAHLLSOPTRYVI
LVAHAMSAISRPSIILGAHTVTINGSSARTHEAERNSTVERSTHVLKAASSPKSPKSP
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EVRRWLLSPEDIGKELGRGKEGHVYLAREKRSNHIVALKVLFKSQLKQSQVBHQLRRE
BELGSHLRHPNILRLYGTVFTWYLILEBYALKGELYKELQRCKHFSERRSATVIASL
AHALIYLHGKHVIHRDIKPBNLLIGSGGELKIADFGWSVHFFNRRRTMCGTLDYLPPP
MVEKTEHDYHVDIWSLGILCYEFLYGVPPFEAKEHSETYRRIVKVDLKFPLKPFVSPA
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                                                                                                                                                                                                                      8354. 8572)

Gene="P0671B11.1"

Join(2314. 2477.3897. .4069,4075. .4227,4366. .4489,

5212. .5449,5890. .5936,5989. .6115,6223. .6423,6713.

7008. .7079,7161. .7292,7386. .7427,7516. .7740,8028.
                                                                                                    oin(2314. .2477,3897. .4069,4075. .4227,4366. .4489,5212. .5449,5890. .5936,5989. .6115,6223. .6423,6713.008. .7079,7161. .7292,7386. .7427,7516. .7740,8028.
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/protein_id="BaB12688.1"
/db_xref="G1:9988422"
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/gene="P0671B11.1"
/note="contains ESTs
AU068014(C11507),C28532(C61484),AU090544(C61415)"
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phosphofructo-1-kinase"
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/db_xref="G1:9988420"
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                                                                   /clone="P0671B11"
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                                                                                                                                                                                         D 162176 IGGTAGTCCGGTCAAACCTTGACATGATTACTCTTGAGAAGTCATTGCCTCCAGATGTTA 162117
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                                                                                                                                                                                                                                                         162116 TCAAGCAGATTATTGATGCACGCCTAAGCCTCGGATTAATTTCACCAGAAAACAAGGGAT 162057
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                                                                                                                      900
                                                                                    Db 162296 TGCAGCGGCGTCTCCTTGATGATCTTGATAAGGTTGAGGTAGATAACCTTCTATTGATCT
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                                                                                                                      841 TATCTGTTGCAAACATTTGTGGTAAAGCATGCGAGAGTTGCTTTCAAGCTGCATTGAGA
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              DB 8;
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            Score 376.4; DB 8
Pred. No. 4.5e-86;
0; Mismatches 276
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AR087501
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Uknes, S.Joseph, Hunt, M.Denise, Steiner, H. and Ryals, J.Andrew. Altered forms of the NIMl gene conferring disease resistance
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Patent: US 5986082-A 1 16-NOV-1999;
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ALQLLSNSFESVFDSPDDFYSDAKLVLSDGREVSFHRCVLSARSSFFKSALAAAKKEK
                                                                                                                                                                                                                                                                                                                                                                                                                     thale cress.

Arabidopsis thaliana
Brayophyta; Embryophyta; Tracheophyta;
Spermatophyta; Wagnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

I (bases 1 to 5655)
Ryals,J., Weymann,K., Lawton,K., Friedrich,L., Ellis,D.,
Steiner,H.-Y., Johnson,J., Delaney,T.P., Jesse,T., Vos,P. and
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4026
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                                                                 ATCGCAAAACAAGCCACTATGGCGGTTGAATGTAATAATATCCCGGAGCAATGCAAGCAT
                                                  CTTTTAACCAAAGGAGGTAGACCTTCTGATCTGACATCCGATGGAAGAAAAGCACTTCAA
                                                                                                    Ryals,J., Weymann,K., Lawton,K., Friedrich,L., Ellis,D.,
Steiner,H.-Y., Johnson,J., Delaney,T.P., Jesse,T., Vos,P.
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.4162,4271. .4474,4586.
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Submitted (29-JAN-1997) Fungicides, Novartis
Road, Research Triangle Park, NC 27709, USA
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/gene="nim1"
join(2787. .3347,3427. .4162,4271.
/gene="nim1"
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join(2754. .3347,3427. .416
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homolog"
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/db_xref="GI:1916912"
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LLDRCKELIVEKSNVDMVSLEKSLPEELVEI IDRREGLEUFVKYKRHVSNVHRALDS
DDIELWELLKEDHTWLDDACALHFAYAYCHVTATDLIKLDLADVHHRNPRGYTVLH
VAAMKEPOLILSLLEKGASASEATLEGRTALMIAKQATMAVECNNIPEQCKHSLKGR
LCVEILLEGEBKREQIPHDYPPSFAVAADELKWTLLDLENRVALAQRIFPRAQAMEI
AEMKGYCEFIVTSLLEPRRIFFRISTSCWKIAPFRILEEHGSRALASTYTEAGR
PRESAVLLOGINNCEDLTQLACGEDDTAEKRLOKRYMEIGETKKAFSSEDNLELGNS
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                                                                                                                                                                                                                                                                                                                                                                                                                                        475 CGGTGCACCGGTGCATTTTGTCGCGAGGAGTCCGTTCTTTAAGAATTTGTTCTGCGGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 577 IGAAAGACCATGAGGTGAGCTATGATGCTGTAATGAGTGTATTGGCTTATTTGTATAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTAAAGTTAGGCCTTCACCTAAAGATGTGTGTTTTGTGTGGACAATGACTGCTCTCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGATCCCTGAATTAATTACTCTCTATCAGGTAAAACACCATCTGCATTAAGCTATGGTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       978 TCACGAGCGGAACTIGGTCTACAAGGGCCTGAAAGCAACGGTTTTCCTGATAAACATGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GATATTCTTGACAAAACTGCAGCAGACGATGTAATGATGGTTTTATCTGTTGCAAACATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGTGGTAAAGCATGCGAGAGTTGCTTTCAAGCTGCATTGAGATTATTGTCAAGTCTAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTTGATATCATAACCCTTGATAAAGCCTTGCCTCATGACATTGTAAAACAAATTACTGAT
                                                                                                                                                                                                                                                                      Length 5655;
                                                                                                                                                                                                                                                           Ouery Match
15.0%; Score 326.8; DB 8;
Best Local Similarity 58.6%; Pred. No. 2.7e-73;
Matches 714; Conservative 0; Mismatches 392;
                                                                                                                                                                               SLTDSTSSTSKSTGGKRSNRKLSHRRR"
                                                                                                                                                                                                      1814 t
                                                                                                                                                                                                    1069 q
                                                                                                                                                                                                  1014 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGATCTCTGAAT - - - - -
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Genes with

음 ò g ò a ò g õ g δ q

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DPKISYNANQLESFAVSNNTANFSFSOYVAVRNPNRAVFSHYDSSIQLLYSGNQVGFM
FIPAGKIDSGRIQYMAATFTVHSFPISPSSAISTVSAAVIPDSFIIPGPPDFTVTP
RNPDSPYFPGYPESPOLLGGNCSPDESGNPGPPSFRNPGSPEFPGNGAPIIPRNPG
SPEFPINPRNPGAPVIPRNPNPPVFPGNPSMGPPGFPGIGGPPGFPGGGGTG
PTLGDGYANPGFGYGNRVGPTMEIESKMELAGRVKVLHVFTHHVVAKSDCRVTVSIAD
GSVLGFHC"
                                                                            or EST similarity are named as unknown proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as thypothetical proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats are identified by repeatmasker (Arian Smit, http://ftp.genome.washington.edu/RM/Repeatmasker.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product-"hypothetical protein; 887-1915"
/protein_id="AAG51715.1"
/db_xref="G1:12323476"
/translation="MAKPHDRRRSSGRTNLASCAVATVFLLILLVVLLVVYFTVFKPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(3199. .3435)
/rpt_family="SIMPLEGUY1|SIMPLEGUY1 is a
putative non-autonomous DNA transposon - a consensus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(3271. 3487)
/rpt_family="SIMPLEGUY1|SIMPLEGUY1 is a
putative non-autonomous DNA transposon - a consensus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(3063. .3486)
/rpt_family="SIMPLEGUY1|SIMPLEGUY1 is a putative non-autonomous DNA transposon - a consensus."
                         similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA transposon - a consensus.
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/rpt_family="SIMPLEGUY1 | SIMPLEGUY1 is a putative non-autonomous DNA transposon - a consensus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /rpt_family="SIMPLEGUY1|SIMPLEGUY1 is a putative non-autonomous DNA transposon - a consensus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(3066. 3493)
/rpt_family-"SIMPLEGUY1 (SIMPLEGUY1 is a putative non-autonomous DNA transposon - a consensus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA transposon - a consensus
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/rpt_family="SIMPLEGUY1|SIMPLEGUY1 is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(3068..3387)

Trpt_family="SIMPLEGUY1 SIMPLEGUY1 is a putative non-autonomous DNA transposon - a consensu complement(3068..3281)

Trpt_family="SIMPLEGUY1 SIMPLEGUY1 SIMPLEGUY1 is a putative non-autonomous DNA transposon - a consensu complement(3196..3285)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /rpt_family="SIMPLEGUY1|SIMPLEGUY1 is a putative non-autonomous DNA transposon - a consens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(3297. .3487)
/rpt_family="SIMPLEGUY1|SIMPLEGUY1 is
putative non-autonomous DNA transposon - a consen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /rpt_family="SIMPLEGUY1|SIMPLEGUY1 is putative non-autonomous DNA transposon - a consen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(3196. .3285)
/rpt_family="SIMPLEGUY1|SIMPLEGUY1
putative non-autonomous DNA transposon - a con
the level of evidence for their annotation.
                                                                                                                                                                                                                                                                                                                                                                    /organism="Arabidopsis thallana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genscan+"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3462)
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                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="predicted by
                                                                                                                                                                                                                                                                                                                                                                                              /cultivar="Columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="F15H21.17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /qene="F15H21.17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="F15H21.17'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (3305.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (3367
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /chromosome="1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="F15H21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .>1915
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDS
                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Sosidae; eurosida II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 96887)
Lin,X., Kaul,S., Town,C.D., Benito,M.-I., Creasy,T.H., Haas,B.J., Mub., Malti,R., Ronning,C.M., Koo,H., Fujii,C.T., Utterback,T.R., Barnstead,M.E., Bowman,C.L., White,O., Nierman,W.C. and Fraser,C.M. Arabidopsis thaliana chromosome 1 BAC F15H21 genomic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genes were identified by a combination of several methods: Gene prediction programs including Genscan+ (Chris Burge, http://CGR-081.mit.edu/GBNSCAN.html), GeneMarkHmM (Mark Borodovsky, http://genemark.biology.gatech.edu/GeneMark/), GlimmerA (a variant of GlimmerM, see Mihaela Pertea, http://www.tigr.org/softlab/glimmerm_htm/glimmerm.html, and GeneSplicer (Mihaela Pertea and Steven Salzberg, contact mpertea@tigr.org), searches of the complete sequence against a peptide database and the plant EST database at TIGR (http://www.tigr.org/tdb/tgi.shtml). Annotated genes are named to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLN 19-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1517
                                                                                                                                                                                                                                                        1457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1278 CTTTTAACCAAAGGAGCTAGACCTTCTGATCTGACATCCGATGGAAGAAAAGCACTTCAA 1337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC066689 96887 bp DNA linear PLN 19-JAN
Arabidopsis thaliana chromosome 1 BAC F15H21 genomic sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Medical Center Dr. Rockville, MD 20850, USA, cdtcwn@tlgr.org
On Jan 19, 2001 this sequence version replaced gi:12280769.
Address all correspondence to:at@tigr.org
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for Genomic Research,
   3787 GTGAAGACCGCAACAGATCTTTTAAAACTTGATCTTGCCGATGTCAACCATGAGAATCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1458 CTAGGAGAAGCTTCTGTATCTCTTGCTATGGCAGGCGATGATTTGCGTATGAAGCTGTTA
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                                                                                               1218 AGGGGATACACGGTGCTGCATGTTGCAGCCATGAGAAAAAGAGCCTAAAATTGTAGTGTCC
                                                                                                                               3967 ATCGCAAAACAAGCCACTATGGCGGTTGAATGTAATAATATCCCGGAGCAATGCAAGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC066689.5 GI:12323462
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Lin, X. and Kaul, S.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1518 TACCTTGAAAATAGAGTT 1535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complete sequence.
AC066689
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VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

JOURNAL

TITLE

JOURNAL AUTHORS REFERENCE TITLE

REFERENCE AUTHORS JOURNAL

COMMENT

DEFINITION RESULT 15 AC066689

ACCESSION

consensus."

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           577 IGAAAGAGCAIGAGGIGAGCIAIGAIGCIGIAAAIGAGIGIATIGGCIITAITIGIAAIAGIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTAAAGTTAGGCCTTCACCTAAAGATGTGTGTGTTTGTGTGGACAATGACTGCTCTCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88679 GCAGAGTGAGACCGCCGCCTAAAGGAGTTTCTGAATGCGCAGACGAGAATTGCTGCCACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTTGATATCATAACCCTTGATAAAGCCTTGCCTCATGACATTGTAAAACAAATTACTGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGTGGTAAAGCATGCGAGAGATTGCTTTCAAGCTGCATTGAGATTATTGTCAAGTCTAAT
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                                                                                                                                                                                                                                                                                                                                                                           96887
                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                           /product="unknown protein; 11471-16325"
/protein_id="AAG51717.1"
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                                                                                                                                                                                                                                                                                                                                                                        Score 326.8; DB 8;
Pred. No. 2.8e-73;
0; Mismatches 392;
      15418. .16325)
/gene="F15H21.18"
/codon_start=1
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58.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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Best Local S
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. .>10294))
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12686. .12786,13367. .13702,13835. .13925,14904. .15298,
                                                                                                                                                                                                                                                                                                     /rpt_family="SIMPLEGUY1|SIMPLEGUY1 SIMPLEGUY1 is a putative non-autonomous DNA transposon - a consensus." complement join <4109. .4202.4301 .4392,4524 .4666, 4711 .4789,5171 .5398,5484 .5585,5691 .5826,6091 .6140,6390 .>6572))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .6140
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RLVLSPSYGDRSRDSVGSAADVSSSILDDELLSSVSAVRDADEALAMISDRFGSNRGG
IVELEDCRSIISAAVSRGNVDLALSIFYTMRASFDLGTLISTLLLTQSGSDNDRWSWS
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AQPQHGVOLYUSCANORYQYELFSGDITSIDSBELGSRGKVIQLMLGVRAVFVQTPSGT
ARTHRPATETAELPAQEGERYIIASAAPSNVV KROVGPPKGTSKAPNFYGEBRNSLTKH
KDGRESILLRPPSKOGDKILQPSFLIPLIAILATGARGASGVIDPSLPQLLSVATVTSL
AIGATLPRRTVDVGIKQQLLSQYDVLQRRIRDLKEAVEKEWMLARMOQLSWILLA
AIGATLPERTVDVGIKQLLSQYDVLQRRIRDLKEAVEKEWMLARMOQLSWILLA
GEPARRTRRVKKRESLENSIKGKIDLIDSYARISSMIEIEVEMDSDVLAARANN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MVGNILVTGGAGYIGSHTVLQLLLGGYNTVVIDNLDNSSLVSIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EDICRDVQRGDPEWRIIMLRYFNPVGAHPSGRIGEDPCGTPNNLMPYVQQVVVGRLPN
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NNNLIATITLLEVMAAHGCKKLVFSSSATVYGWPKEVPCTEESPLSGMSPYGRTKLFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LKIYGTDYTTKDGTGVRDYIHVVDLADGHICALQKLDDTEIGCEVYNLGTGKGTTVLE
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12686. .12786,13367. .13702,13835. .13925,14904. .15298,
15418. .>16325)
/gene="F15H21.18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="similar to GI:3021357 from [Cyamopsis tetragonoloba] (Plant Sci. 142, 147-154 (1999))" complement(join(4109. 4202.4301. .4392,4524. .4606,4711. .4789,5171. .5398,5484. .5585,5691. .5826,6091. .6372) /gene="F15H21:11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(join(7338. .7400,7552. .7605,7688. .7759,7853. .7940,8028. .8095,8180. .8287,8409. .8792,9058. 9145. .9244,9310. .9387,9478. .9629,9686. .10133))
                                                                                                                                                                                                                                   /rpt_family="SIMPLEGUY||SIMPLEGUY1 SIMPLEGUY1 is a putative non-autonomous DNA transposon - a consensus.complement(3385, .3487)
      - a consensus.
                                                                                        - a consensus
                                                                                                                                                                                    - a consensus.
                      complement(3384. .3494)
/rpt_family="SIMPLEGUY1|SIMPLEGUY1 is a
putative non-autonomous DNA transposon - a consensu
                                                                                                                              /rpt_family="SIMPLEGUY1|SIMPLEGUY1 SIMPLEGUY1 putative non-autonomous DNA transposon - a concomplement(3384, 3459)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TENIAQQIEQIMELENLEEKWKIQAEANDEAERLLSSQP"
DNA transposon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="unknown protein; 10133-7338"
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/db_xref="G1:12323467"
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1741 TTGGAAAACGCTTCTTTCCACGTTGTTCAGAAGTTCTAAATAAGATCATGGATGCTGATG 1800
                                                                                                                                                                                                                                                                   Systemic acquired resistance; SAR; signal transduction cascade; disease resistance; tobacco; tomato; canola; sunflower; sugarbeet;
                    ACTIGICTGAGATAGCTTACATGGGGAATGATACGGCAGAGAGGGGGTCAACTGAAGAAGC
                                      AAAGGTACATGGAACTTCAAGAAATTCTGACTAAAGCATTCACTGAGGATAAAGAAAT
                                                               ATGATAAGACTAACAACATCTCCTCATCTTGTTCCTCTACATCTAAGGGAGTAGATAAGC
                                                                                         Novel plant genes for enhancing systemic acquired resistance gene expression and broad spectrum disease resistance in plants, are homologues of Arabidopsis NIM1 gene -
                                                                                                                                                                                                                                                       N. tabacum NIM1 homologue coding sequence SEQ ID NO: 1.
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                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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P-PSDB; AAB27301.
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                and their coding sequences from Arabidopsis thalians, Brassica napus, Nicotiana tabacum, Lycopersicon esculentum, Beta vulgaris, Helianthus annus and Solanum tuberosum. NIM1 is one of the proteins involved in the signal transduction cascade leading to systemic acquired resistance (SAR) in plants. This gives the plants an increased resistance to disease. The gene and protein can be used to produce transgenic plants resistant to diseases caused by viruses, such as tobacco or cucumber mosaic virus, ringspot virus, pelargonium leaf curl virus, red clover mottle virus, tomato bushy stunt virus, fungi, including Phythophthora parasitica and Peronospora tabacina, bacteria such as secudomonas syringae and Peabach, insects, including aphids and lepidoptera and nematodes such as Meloidogyne incognita. In particular they can be used against disease
present invention is concerned with the isolation of NIM1 homologues
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Mismatches
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             GGAAGAAAAGCACTTCAAATCGCCAAGAGGCTCACTAGGCTTGTGGATTTCAGTAAGTCT
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       TTTCCTGATAAACATGTTAAGAGGATACATAGGGCCATTGGATTCTGATGTGTTGAATTA
                                 CTACAAATGTTGCTAAGAGAGGGGCATACTACCCTAGATGATGCATATGCTCTCCATTAT
                                                                           GCTGTAGCGTATTGCGATGCAAAGACTACAGCAGAACTTCTAGATCTTGCACTTGCTGAT
                                                                                         ATTAATCATCAAAATTCAAGGGGATACACGGTGCTGCATGTTGCAGCCATGAGAGAG
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The present invention is concerned with the isolation of NIMI homologues and their coding sequences from Arabidopsis thaliana, Brassica napus, Micotiana tabacum, Lycopersicon esculentum, Beta vulgaris, Helianthus annuus and Solanum tuberosum. NIMI is one of the proteins involved in the signal transduction cascade leading to systemic acquired resistance (SAR) in plants. This gives the plants an increased resistance to disease. The gene and protein can be used to produce transgenic plants resistant to diseases caused by viruses, such as tobacco or cucumber mosaic virus, ringspot virus, pelargonium leaf curl virus, red clover mottle virus, remato bushy stuft virus, fungi, including Phythophthora parasitica and Peronospora tabacina, bacteria such as Pseudomonas syringae and P. tabacii, insects, including aphids and lepidoptera and nematodes such as Meloidogyne incognita. In particular they can be used against disease
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                                                                                                                    disease resistance; tobacco; tomato; canola; sunflower; sugarbeet;
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ssion and broad spectrum disease resistance in plants, are
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                                                                                             Systemic acquired resistance; SAR; signal transduction cascade;
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                                              ID NO:
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                                              esculentum NIM1 homologue coding sequence SEQ
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(NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
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ilarity 88.4%;
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AAA97191 standard; cDNA; 1731

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                                                                       TAATGAGIGTATTGGCTTATTGTATAGTGGTAAAGTTAGGCCTTCACCTAAAGATGTGT
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1295 CAAAAGTTGCAATGGACATTGCACAAGTTGATGGCACGTCTGAATTACCCCTGGCTAGCA
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(NOVS ) NOVARTIS-ERFINDUNGEN VERW GES
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P-PSDB; AAB27324.
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nover plant genes for enhancing systemic acquired resistance gene expression and broad spectrum disease resistance in plants, are homelogines of harbidocals with a second panes. homologues of Arabidopsis NIM1 gene -

Claim 3; Page 127-130; 152pp; English.

The present invention is concerned with the isolation of NIMI homologues and their coding sequences from Arabidopsis thaliana, Brassica napus, Nicotiana tabacum, Lycopersicon esculentum, Beta vulgaris, Halianthus annuus and Solanum tuberosum. NIMI is one of the proteins involved in the signal transduction cascade leading to systemic acquired resistance (SAR) in plants. This gives the plants an increased resistance to disease. The gene and protein can be used to produce transgenic plants resistant to diseases caused by viruses, such as tobacco or cucumber mosaic virus, ringspot virus, pelargonium leaf curl virus, red clover mottle virus, tomato bushy stunt virus, fungi, including Phythophthora parasitica and Peronospora tabacina, bacteria such as Pseudomonas syringae and P. tabaci, insects, including aphids and lepidoptera and nematodes such as Mallidgagne incognita. In particular they can be used against disease organisms of maize. 

Sequence 2299 BP; 644 A; 483 C; 510 G; 662 T; 0 other;

4; ATAGTAGGACTGCGTTTTCTGATTCGAATGACATCAGCGGAAGCAGTAGTATATGCTGCA 306 203 263 408 468 383 443 585 503 627 563 687 623 747 683 807 867 803 CATGCGAGAGATTGCTTTCAAGCTGCATTGAGATTATTGTCAAGTCTAATGTTGATATCA 927 354 Gaps **ACAAAA**CTGCAGCAGACGATGTAATGATGGTTTTATCTGTTGCAAACATTTGTGGTAAAG ACAAGATTGCACCAGATGACGTTCTAGTAGTGTTATCTGTCGCTGAGATGTGTGGAAATG ATTOTOGOACCGCTTTCTCCGATTCCAACGACATCAGCAATGGCAGTAGCATCTGCTGCG TCGGCGGCGCCATGACTGTATTTTTCTCGCCGGAGA------CTTCGCCGGCGG ACGCCCCCCTCTTCTCCCCCTCTCTGAAACCTCGACTCCCTTTTCCAACCTCGCTTT **AAATTCCGGTGCACCGGTGCATTTTGTCGGCGAGGAGTCCGTTCTTTAAGAATTTGTTCT** ------ATGAGGTGAGCTATGATGCTGTAATGAGGTGTATTG TGTATAGTGGCAAAGTTAGGAATTTGCCTAGAGGAATTTGTGTTTTGTGTTGATGAGGATT GCTCTCATGTGGCTTGTAGGCCAGCTGTGGCATTCCTGGTTGAGGTTTTGTACACATCAT TTACCTTTCAGATCTCTGAATTGGTTGACAAGTTTCAGAGACACCTACTGGATATTCTTG ---GT CTTTGCCGGAGTTTGACTACTTCGCCGACGCTAAGCTTGTGGTTTCCGGCCCGTGTAAGG 48; DB 21; Length Indels Score 781.2; DB 21; Pred. No. 3.1e-201; 0; Mismatches 528; Query Match 36.0%; Best Local Similarity 67.3%; Matches 1186; Conservative 247 529 748 744 898 144 264 324 469 384 444 564 624 308 307 204 355 409 586 628 889 g ò a ò g ò 셤 ò g ò g ò g ò a ò g ò g à 셤 ò

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CICCATTATGCTGTAGCGTATTGCGATGCAAGACTACAGGCAGAACTTCTAGATCTTGCA 1190
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99US-0123548.
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09-MAR-1999;
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25-MAR-1999;
29-MAR-1999;
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16-APR-1999;
19-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel plant genes for enhancing systemic acquired resistance gene expression and broad spectrum disease resistance in plants, are homologues of Arabidopsis NIM1 gene -
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Pred. No. 5.8e-158;
0; Mismatches 24;
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                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
1875 CGTCGTCGTCGACTCCAATGGG 1896
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ilarity 96.4%;
Conservative
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                                                                                                                                                                                                                                                               potato; ds.
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Query Match

Local Matches

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UUS-0130449 UUS-0130510 UUS-0130891 UUS-0131449 UUS-0132484 UUS-0132484 UUS-0132484 UUS-0132487 UUS-0132487 UUS-0132487 UUS-0132487 UUS-0132487 UUS-0132487	990S-0134370. 990S-0134941. 990S-0134941. 990S-0135124. 990S-0135623. 990S-0136021. 990S-0137222. 990S-0137222. 990S-0137222. 990S-0137222. 990S-0137222. 990S-013724. 990S-013945. 990S-013945. 990S-013945. 990S-013945. 990S-013945. 990S-013945. 990S-013945. 990S-013945.	90GS - 0139463 90GS - 0139463 90GS - 0139763 90GS - 0140354 90GS - 0140354 90GS - 0140991 90GS - 0140991 90GS - 0141287 90GS - 014287 90GS - 0142803 90GS - 0142803 90GS - 0142803 90GS - 014290 90GS - 014390 90GS - 0144390 90GS - 0144986 90GS - 0144986 90GS - 0144986 90GS - 0144334 90GS - 0144334 90GS - 0144334 90GS - 0144334 90GS - 0144334 90GS - 0144334
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PR 20-JUL-1999; 99US-0144532.

PR 20-JUL-1999; 99US-0144684.

PR 21-JUL-1999; 99US-0144884.

PR 21-JUL-1999; 99US-0145086.

PR 22-JUL-1999; 99US-0145088.

PR 22-JUL-1999; 99US-0145089.

PR 22-JUL-1999; 99US-0145089.

PR 22-JUL-1999; 99US-0145089.

PR 22-JUL-1999; 99US-0145145.

PR 22-JUL-1999; 99US-0145145.

PR 23-JUL-1999; 99US-014514.

PR 23-JUL-1999; 99US-014514.

PR 23-JUL-1999; 99US-014514.

PR 23-JUL-1999; 99US-014514.

PR 23-JUL-1999; 99US-014518.

PR 23-JUL-1999; 99US-014518.

PR 23-JUL-1999; 99US-0149175.

PR 23-JUL-1999; 99US-011908.

PR 23-JUL-1999; 99US-011908.

PR 23-JUL-1999; 99US-011908.

PR 23-JUL-1999; 99US-011908.

PR 23-SEP-1999; 99US-0119183.

PR 23-SEP-1999; 99US-011540.

PR 23-SEP-1999; 99US-011540.

PR 23-SEP-1999; 99US-011540.

PR 23-SEP-1999; 99US-01540.

PR 23-SEP-1999; 99US-015775.

PR 23-SEP-1999; 99US-015775.

PR 23-SEP-1999; 99US-015786.

PR 23-SEP-1999; 99US-015786.

PR 23-SEP-1999; 99US-015782.

PR 23-SEP-1999; 99US-015775.

PR 23-SEP-1999; 99US-015782.

PR 24-SEP-1999; 99US-015782.

PR 26

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                                                                                                                                                                                                                                                                                                                                                                                              GCCTGGCTAAAACTCCTTTTTCCAATGGAAGCTAAAGTTGCAATGGACATTGCTCAAGTTG
                                           ATGATGCATATGCTCCCATTATGCTGTAGCGTATTGCGATGCAAAGACTACAGCAGAAC
                                                        TTCTAGATCTTGCACTTGCTGATATTAATCAAAATTCAAGGGGATACACGGTGCTGC
                                                                                                                                                                                                                                             GGCTTGTGGATTTCAGTAAGTCTCCGGAGGAAGGAAAATCTGCTTCGAATGATCGGTTAT
                                                                                                                                                                                                                                                           GACCTTCTGATCTGACATCCGATGGAAGAAAAGCACTTCAAATCGCCAAGAGGCTCACTA
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                                                                                                                                                                                                                                                                                                             CTCTTGCTATGGCAGGCGATGATTGCGTATGAAGCTGTTATACCTTGAAAATAGAGTTG
                                                                                                                                                                                                                                                                                                                                                                       CTTTTGCAGTGGCGCCGATGAATTGAAGATGACGCTGCTCGATCTTGAAAATAGAGTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                ATGGCACTTCTGAGTTCCCACTGGCTAGCATCG---GCAAAAAGATGGCTAATGCACAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1057 TGGATTCTGATGTTGAATTACTACAAATGTTGCTAAGAGGGGGCATACTACCTAG 1116
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                                                                                                                                                                                                                                                                                                                                                                                                   CGGTGCACCGGTGCATTTTGTCGGCGAGGAGTCCGTTCTTTAAGAATTTGTTCTGCGGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAAAGGAGAAATAGTAGT--------AAAGGTGGAATTGAAGGAGGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGAAAGAGCATGAGGTGAGCTATGATGCTGTAATGAGTGTATTGGCTTATTTGTATAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCAAGGATTACGAAGTCGGTTTCGATTCGGTTGTGACTGTTTTGGCTTATGTTTACAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTAAAGTTAGGCCTTCACCTAAAGATGTGTGTGTTTGTGTGGACAATGACTGCTCTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GATTGCTTTCAAGCTGCATTGAGATTATTGTCAAGTCTAATGTTGATATCATAACCCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATAAAGCCTTGCCTCATGACATTGTAAAACAAATTACTGATTCACGAGCGGAACTTGGTC
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                                                                                                                                                                                                                                                                                                         Length 2024;
                                                                                                                                                                                                                                                                                                      DB 21;
                                                                                                                                                                                                                                                                                                                               544;
                                                                                                                                                                                                                                                                                                     Score 581.6; DB 27
Pred. No. 3.7e-147,
0; Mismatches 544,
990S-0159331.
990S-0159637.
990S-0159538.
990S-0160741.
990S-0160767.
990S-01607768.
                                                                                                              99US-0160815.
99US-0160980.
99US-0160981.
                                                                                                                                                990S - 0160989
990S - 0161404
990S - 0161406
990S - 0161406
990S - 0161359
990S - 0161360
990S - 0161920
990S - 0161992
990S - 0161992
                                                                                                                                                                                                                                                                                                     26.8%;
62.9%;
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                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                 Similarity
14-0CT-1999;
14-0CT-1999;
18-0CT-1999;
21-0CT-1999;
21-0CT-1999;
21-0CT-1999;
21-0CT-1999;
                                                                                              21-0CT-1999;
22-0CT-1999;
22-0CT-1999;
22-0CT-1999;
25-0CT-1999;
25-0CT-1999;
26-0CT-1999;
26-0CT-1999;
26-0CT-1999;
                                                                                                                                                                                                                                                  28-OCT-1999;
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                                                                                                                                                                                                                                                                                                                             984;
                                                                                                                                                                                                                                                                                                      Match
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Matches
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us-08-908-884-13.rng

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the encoded
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence is that of the acquired resistance gene NPRI. It may be used in the production of transgenic cells which can produce the enco acquired resistance protein. Such transgenic plants cells are useful in the production of plants having an increased level of resistance against disease caused by plant pathogens, e.g. bacteria, mycoplasmas, fungi, insects, nematodes, viruses, and viroids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGGAGITIGACTACTTCGCCGACGCTAAGCTTGTGGTTTCCGGCCCGTGTAAGGAAATTC 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
       pathogens; bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGGTGCACCGGTGCATTTTGTCGCCGAGGAGTCCGTTCTTTAAGAATTTGTTCTGCGGTA
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                                                                                                                                                                                                                                                                                                                                                                              New isolated plant acquired resistance polypeptide gene - useful for, e.g. producing plants with increased resistance to pathogens such as bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 19; Length 2104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
 ..... yeue; acquired resistance; disease; plant pathogens mycoplasma; fungi; insects; nematodes; viruses; virolds; transgenic; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2104 BP; 606 A; 431 C; 482 G; 585 T; 0 other;
                                                                                                         /*tag= a
/product= acquired resistance protein
/note= NPR1 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 578.4; DB 19;
Pred. No. 2.8e-146;
0; Mismatches 546;
                                                                                                                                                                                                                                                                                                                      ь,
;
                                                                                                                                                                                                                                                                                                                      Glazebrook
                                                                         Location/Qualifiers
93..1874
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62.8%;
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                                                                                                                                                                                                                                 97US-0046769
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                                                          thaliana
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P-PSDB; AAW46940.
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                                                                                                                                                                                                                                                                                 (GEHO ) GEN HOSPIT
(UYDU-) UNIV DUKE.
                                                                                                                                                                                                         38-AUG-1997;
                                                                                                                                                           WO9806748-A1
                                                                                                                                                                                                                                 16-MAY-1997;
                                                          Arabidopsis
                                                                                                                                                                                                                                              39-AUG-1996;
                                                                                                                                                                                                                                                                                                                      Ausubel FM,
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Matches 982;
                                                                                                                                                                                                                                                        10-JAN-1997
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This protein is used in a method resulting in the protection of an immunomodulated plant having a first level of resistance and involves treatment with at least 1 microbicide that confers a second level of resistance, such that the plants have a third level of resistance greater than the sum of the first two levels. The method can be applied to a wide variety of plants (cereals, fruits, oilseeds, vegetables etc.) to protect against viruses, fungi, bacteria, insects and namarodes. The method provides a high level of resistance and allows a reduction in the amount of micobicide used. Since the process involves two different methods of protection, it is unlikely that the pathogen will develop resistance to
                                                                           1834 CGGCAGAAGAGCGTCAACTGAAGAAGCAAAGGTACATGGAACTTCAAGAAATTCTGACTA 1893
               SAR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This cDNA sequence encodes the NIM-1 protein from Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                    NIM-1; noninducible immunity; systemic acquired resistance; SAR; pathogen; disease; protection; immunomodulated; plant; cereal; fruit; vegetable; virus; fungi; bacteria; insect; nematode; microbicide; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protection of immunomodulated plants against pathogens - comprises applying microbicide to provide increase in resistance
                                                          AAGCATTCACTGAGGATAAAGAAGAATATGATAAGACTAACAACATCTCCTCATCTTGTT
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96US-0034378
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                                                                                                                                                                                                                                                                                                          A. thaliana NIM-1 cDNA.
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Score 576.8; DB 19; Length 2011; Pred. No. 7.3e-146;

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Best Local Similarity

Query Match

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                                                                                                                                                                                                                              CGGCAGAAGAGGGTCAACTGAAGAAGCAAAGGTACATGGAACTTCAAGAAATTCTGACTA 1893
                                                                                                                                                                                                                                       1643 CTGCTGAGAAACGACTACAAAAGAAGCAAAGTACATGGAAATACAAGAGACACTAAAGA 1702
                                                                                                                                                                                                                                                                  AAGCATTCACTGAGGATAAAGAAGAATATGATAAGACTAACAACATCTCCTCATCTTGTT 1953
                                                                                                                                                                                                                                                                            1703 AGGCCTTTAGTGAGGACAATTTGGAATTAGGAAATTTGTCCCTGACAGATTTGACTTCTT 1762
                                                                                                                                                                                                                                                                                                                                                                                                                                        NIM-1; noninducible immunity; systemic acquired resistance; SAR; pathogen; disease; protection; immunomodulated; plant; cereal; fruit; vegetable; virus; fungi; bacteria; insect; nematode; microbicide; ss.
          CTCTTGCTATGGCAGGCGATGATTTGCGTATGAAGCTGTTATACCTTGAAAATAGAGTTG
                   1283 CTTTTGCAGTGGCGGCCGATGAATTGAAGATGACGCTGCTCGATCTTGAAAATAGAGTTG
                                                       ATGGCACTICTGAGTTCCCACTGGCTAGCATCG----GCAAAAAGATGGCTAATGCACAGA
                                                                                            GGACAACAGTAGATTTGAACGAGGCTCCTTTCAAGATAAAAGAGGAGCACTTGAATCGGC
                                                                                                                                                        TTAGAGCACTCTCTAGAACTGTAGAACTTGGAAAACGCTTCTTTCCACGTTGTTCAGAAG
                                              GCCTGGCTAAACTCCTTTTTCCAATGGAAGCTAAAGTTGCAATGGACATTGCTCAAGTTG
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/note= "wild type TCG is
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/note= "wild type TCC is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                       A. thaliana NIM-1 cDNA variant #1.
                                                                                                                                                                                                                                                                                                                                                                   AAV46275 standard; cDNA; 2011 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "variant"
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/product= NIM-1
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205..207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
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This sequence encodes a variant NIM-1 protein from Arabidopsis thaliana. This protein is used in a method resulting in the protection of an immunomodulated plant having a first lead of resistance and involves treatment with at least 1 microbicide that confers a second level of resistance, such that the plants have a third level of resistance greater than the sum of the first two levels. The method can be applied to a wide variety of plants (cereals, fruits, oilseeds, vegetables etc.) to protect against viruses, fungi, bacteria, insects and nematodes. The method provides a high level of resistance and allows a reduction in the amount of micobicide used. Since the process involves two different methods of protection, it is unlikely that the pathogen will develop resistance to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           816
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            634
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            415 CGGAGTTTGACTACTTCGCCGACGCTAAGCTTGTGGTTTCCGGCCCGTGTAAGGAAATTC 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      475 CGGTGCACCGGTGCATTTTGTCGCGAGGAGTCCGTTCTTTAAGAATTTGTTCTGCGGTA 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GATTGCTTTCAAGCTGCATTGAGATTATTGTCAAGTCTAATGTTGATATCATAACCCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    535 AAAAGGAGAAATAGTAGT-------AAGGTGGAATTGAAGGAGGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         577 TGAAAGAGCATGAGGTGAGCTATGATGCTGTAATGAGTGTATTGGCTTATTTGTATAGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 576.8; DB 19; Length 2011;
Pred. No. 7.3e-146;
0; Mismatches 547; Indels 36;
                                                                                                                                       SJ;
                                                                                                                                                                                                                                                                      Protection of immunomodulated plants against pathogens applying microbicide to provide increase in resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2011 BP; 563 A; 417 C; 474 G; 557 T; 0 other;
                                                                                                                                       Uknes
                                                                                                                                       Ryals JA,
                                                                                                                                                                                                                                                                                                                                                               Claim 11; Page 116-120; 164pp; English.
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                                                                                                                                          Friedrich LB, Molina Fernandez
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ilarity 62.7%;
Conservative
97US-0035024.
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                                                                                (NOVS ) NOVARTIS AG
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Tue Oct

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1297 GACCTICIGAICTGACAICCGAIGGAAGAAAGCACTICAAAICGCCAAGAGGCICACIA 1356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATGATGCATATGCTCTCCATTATGCTGTAGCGTATTGCGATGCAAAGACTACAGCAGAAC 1176
                                                                                                                                                                          TTCTAGATCTTGCACTTGCTGATATTAATCATCAAAATTCAAGGGGATACACGGTGCTGC 1236
                                                                                                                                                                                                                                                            1043 ATGTTGCTGCGATGCGGAAGGAGCACAATTGATACTATCTCTATTGGAAAAAGGTGCAA 1102
                                                                                                                                                                                                                                                                                                          1403 AGGGAACATGTGAGTTCATAGTGACTTGGCCTGACCGTCTCACTGGTACGAAGA 1462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            997 TACAAGGGCCTGAAAGCAACGGTTTTCCTGATAAACATGTTAAGAGGATACATAGGGCAT 1056
                                                                                                                                                                                                                                  1237 ATGTTGCAGCCATGAGGAAAGAGCCTAAAATTGTAGTGTCCCTTTTAACCAAAGGAGCTA 1296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1894 AAGCATTCACTGAGGATAAAGAAGAATATGATAAGACTAACAACATCTCCTCATCTTGTT 1953
                   1357 GGCTTGTGGATTTCAGTAAGTCTCCGGAGGAAGGAAAATCTGCTTCGAATGATCGGTTAT
                                                                                                                                                                                                                                                                                                                                                                                                           1417 GCATTGAGATTCTGGAGCAGAAGAAGAAGAGACCCTCTGCTAGGAGAAGCTTCTGTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                        1223 GTGTAGAAATACTAGAGCAAGAAGACAAACGAGAACAAATTCCTAGAGATGTTCCTCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTCTTGCTATGGCAGGCGATGATTTGCGTATGAAGCTGTTATACCTTGAAAATAGAGTTG
                                                        1057 IGGATICIGAIGAIGTIGAATIACTACAAAIGTIGCTAAGAGGGGGCATACTACCCIAG
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AAV43661 standard; cDNA; 2011 BP.

RESULT 10 AAV43661

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Inducible immunity-1 (NIM) protein. Sequences shown in AAV43661 to
AAV43665 represent variants of the NIM1 CDNA. The invention provides a
chimeric gene comprising a promoter active in plants operatively linked
to a DNA molecule that encodes an altered form of the NIM1 protein. Plant
cells stably transformed with a recombinant vector comprising such a
chimeric gene have a broad spectrum of disease resistance. The altered
chimeric gene have a broad spectrum of disease resistance. The altered
chimeric gene have a broad spectrum of disease resistance. The altered
chimeric gene have a broad spectrum of disease resistance.
CC chimeric gene have a broad spectrum of disease resistance.
CC acquired resistance (SAR) signal transduction pathway. The transgenic
plants transformed with an altered NIM1 gene exhibits constitutive SAR
expression which is higher in the transformed plants than in a wild-type
plants. The products can be used for producing plants with a broad
compounds that induce constitutive immunity (CIM) phenotype
in plants. The inventions can be used with plants such as rice, wheat,
barley, rye, corn, potato, carrot, sweet potato, sugar beet, bean, pea,
chicory, lettuce, cabbage, cauliflower, broccoli, turnip, radish,
spinach, asparagus, onion, garlic, eggplant, pepper, celery, carrot,
squash, pumpkin, zucchini, cucumber, apple, pear, quince, melon, plum,
cherry, peach, nectarine, apricot, strawberry, grape, raspberry,
blackberry, pineapple, avocado, papaya, mango, banana, soybean, tobacco,
                                                                                                                      Non-inducible immunity-1 gene; NIM1 gene; disease resistance; mutant; transgenic plant; SAR; systemic acquired resistance; CIM; pathogen; constitutive immunity; agriculture; variant; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Use of non-inducible immunity-1 gene - for transforming plants to produce transgenic plants having a broad spectrum disease resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This cDNA encodes an altered form of the Arabidopsis thaliana non
                                                                                   Non-inducible immunity-1 (NIM1) protein variant 1 encoding cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Steiner HY;
                                                                                                                                                                                                                                                                                                                                                                                         /*tag= c
/note= "wild type TCG is replaced by GCG"
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/note= "wild type TGC is replaced by
                                                                                                                                                                                                                                                                                                   "NIM1 protein variant 1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 5; Pages 140-144; 205pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lawton KA,
                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96US-0034382.
97US-0034730.
97US-0035021.
97US-0035022.
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205..207
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                                                                                                                                                                                                                                                                                    /*tag=
                                                                                                                                                                                           Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1998-348536/30.
P-PSDB; AAW61983.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9826082-A1.
                                                  29-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-DEC-1996;
27-DEC-1996;
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10-JAN-1997
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                                                                                                                                                                                                          Synthetic
              AAV43661;
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1283 CTTTGCAGTGGCGCCGATGAATTGAAGATGACGCTGCTCGATCTTGAAAATAGAGTTG 1342
                                                                                                                                                                                                                                                               1583 TGCTCGACCAGATTATGAACTGTGAGGACTTGACTCAACTGGCTTGCGGAGAAGACGACA 1642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GIGCATCAGAAGCAACTTIGGAAGGIAGAACCGCACTCAIGAICGCAAAACAAGCCACTA 1162
                                                                                                                                                                                            GCCTGGCTAAACTCCTTTTTCCAATGGAAGCTAAAGTTGCAATGGACATTGCTCAAGTTG 1596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Systemic acquired resistance; SAR; signal transduction cascade; disease resistance; tobacco; tomato; canola; sunflower; sugarbeet;
                                                  GCATTGAGATTCTGGAGCAAGCAGAAAGAAGAGACCCTCTGCTAGGAGAAGCTTCTGTAT
                                                                                                     GGACAACAGTAGATTTGAACGAGGCTCCTTTCAAGATAAAAGAGGAGCACTTGAATCGGC
                                                                                                                                                                                                                                                                                                                                                      TTAGAGCACTCTCTAGAACTGTAGAACTTGGAAAACGCTTCTTTCCACGTTGTTCAGAAG
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                                                                                                                                         CICITGCTATGGCAGGCGATGATTTGCGTATGAAGCTGTTATACCTTGAAAATAGAGTTG
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tomato, sorghum and sugarcane. The plants produced are resistant to plant pathogens such as viruses, virolds, fungi, bacteria, insects such as aphids and lepidoptera and nematodes. The plants produced can be used in agriculture.
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                                                                                                  Score 576.8; DB 19; Length 2011;
Pred. No. 7.3e-146;
0; Mismatches 547; Indels 36;
                                                                            Sequence 2011 BP; 563 A; 417 C; 474 G; 557 T; 0 other;
                                                                                                   Query Match 26.6%;
Best Local Similarity 62.7%;
Matches 981; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                gene and protein can be used to produce transgenic plants resistant to diseases caused by viruses, such as tobacco or cucumber mosaic virus, ringspot virus, pelargonium leaf curl virus, red clover mottle virus, tomato bushy stunt virus, fungi, including Phythophthora parasitica and Peronospora tabacina, bacteria such as Pseudomonas syringae and Perabaci, insects, including aphids and lepidoptera and nematodes such as Meloidogyne incognita. In particular they can be used against disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTGTAAAACAAATTACTGATTCACGAGGGGAACTTGGTCTACAAGGGGCCTGAAAGCAAC 1016
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel plant genes for enhancing systemic acquired resistance gene expression and broad spectrum disease resistance in plants, are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 TATGCTGTAGCATATTGCGATGCAAAGACTACAGCAGAACTTTTAGATCTTTCACTTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 575.4; DB 21; Length 653;
Pred. No. 1e-145;
2; Mismatches 48; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 653 BP; 200 A; 124 C; 140 G; 187 T; 2 other;
                                                                                                                                   Mengiste T;
                                                                                      ) NOVARTIS AG.
) NOVARTIS-ERFINDUNGEN VERW GES MBH.
                                                                                                                                 Willits MG,
                                                                                                                                                                                                                                     homologues of Arabidopsis NIM1 gene
                                                                                                                                                                                                                                                              Claim 3; Page 115; 152pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26.5%;
92.3%;
                           07-MAR-2000; 2000WO-EP01978.
                                                         99US-0265149
                                                                                                                                 Weislo LJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                           2000-594322/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organisms of maize.
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                                                                                                                                Salmeron JM,
                                                       09-MAR-1999;
14-SEP-2000.
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The invention relates to rice proteins (AAB29749-B29757) and the nucleotides encoding the proteins (AAC81456-C81464), which are involved in the induction of systemic acquired resistance (SAR), a general plant resistance response that can be induced during a local infection by an avirulent pathogen. A rice cDNA library was screened using the yeast two hybrid system with Arabidopsis NRP1 cDNA as bait, and the rice proteins that (proline rich NPR1 interactor; AAB29749) and MN1 (AAB29758) were identified as interacting with Arabidopsis NRP1. The rice cDNA library was then rescreened using rice PNI cDNA or rice MN1 (CDNA as bait, Rice NH1 and NH2 (NPR homologues I and 2; AAB29753), and a protein with no protein (AAB29754) were identified as interacting with PNI protein and rice GRLI and GRLI (glutaredoxin homologues I and 2; AAB29755, AAB29755) and rice MADA1 (a protein with homology to rat microtubule-associated protein; AAB29757) were found to interact with a microtubule-associated protein; AAB29757) were found to interact with a screet of the control of the invention additionally encompasses transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              plants comprising an expression cassette encoding a protein of the invention, and a method for enhancing resistance to pathogens in a plant by introducing the expression cassette into the plant, and selecting the plant with enhanced resistance. The rice SAR-associated nucleic acids and proteins are useful for enhancing plant resistance to pathogens such as viruses, bacteria, nematodes, fungi or insects. The present sequence represents cDNA encoding rice NH1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rice; NH1; NPR1 homologue 1; PNI interactor; SAR; bZIP protein;
systemic acquired resistance; yeast two-hybrid system; transgenic plant;
pathogen resistance; virus; bacterium; nematode; fungus; insect; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   encodes
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TCTCCGGAGGAAGGAAAATCTGCTTCGAATGATCGGTTATGCATTGAGATTCTGGAGCAA
                                          GCAGAAAGAAGACCCTCTGCTAGGAGAAGCTTCTGTATCTCTTGCTATGGCAGGCGAT
                                                                                                                                                                                                          GATITGCGTATGAAGCTGTTATACCTTGAAAATAGAGTTGGCCTGGCTAAACT 1549
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The present sequence is a putative version of the rice negatively phytochrome regulated 1 (NPR1) gene coding sequence. It was isolated by screening a leaf cDNA library for those sequences which were similar to the NPR1 gene from Arabidopsis thaliana. The protein is involved in systemic acquired resistance and this gene can be used to create transgenic plants which are protected from pathogens. It can also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated nucleic acid fragments encoding an NPRI gene which can be used to transform plants and provide disease resistance
                                                                                                                                                                                                        1316 TGGCAAGGATTATGTTTCCGATGGAGGCAAGAGTAGCAATGGATATTGCTCAAGTGGATG 1375
                                                  GAACTITGGAATTTAACCTGGGTTCTGGTGCAAATCCACCTCCTGAAAGACAACGGACAA 1435
                                                                                                                                CACTCTCTAGAACTGTAGAACTTGGAAAACGCTTCTTTCCACGTTGTTCAGAAGTTCTAA 1779
                                                                                                                                              1780 ATAAGATCATGGATGCTGATGACTTGTCTGAGATAGCTTACATGGGGAATGATACGGCAG 1839
                                                                                                                                                                                                                                        1840 AAGAGCGTCAACTGAAGAAGCAAAGGTACATGGAACTTCAAGAAATTCTGACTAAAGCAT 1899
                         GCACTTCTGAGTTCCCACTGGCTAGCATCGGCAAAAAGATGGCTAATGCACAGAGGACAA
                                                                             CAGTAGATTTGAACGAGGCTCCTTTCAAGATAAAAGAGGAGCACTTGAATCGGCTTAGAG
                                                                                         1661 TCCACGAGGACAAGGAGGAGAATGACAGGTCGGGGGCTCTCGTCGTCGTCGTCGTCTTCT 1715
                                                                                                                                                                                                                                                                                             1900 TCACTGAGGATAAAGAAGAATATGATAAGACTAACAACATCTCCTCATCTTGTTC 1954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rice; negatively phytochrome regulated 1 gene; NPR1; systemic acquired resistance; gene mapping; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rice putative negatively phytochrome regulated 1 (NPR1) gene
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                                                                                                                                                   640 AAGTTAGGCCTTCACCTAAAGATGTGTGTGTTTGTGTGGACAATGACTGCTCTATGTGG
                                           2040;
                                                                   15;
                                        Score 563.4; DB 22; Length Pred. No. 3.2e-142; 0; Mismatches 476; Indels
                BP; 501 A; 525 C; 553 G; 461 T; 0 other;
                                          25.9%;
64.3%;
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                                                        Similarity
                Sequence 2040
                                                                    Matches 884;
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                                                          Score 558.6; DB 21; Length
Pred. No. 6.6e-141;
0; Mismatches 479; Indels
                                Sequence 2194 BP; 510 A; 586 C; 617 G; 481 T; 0 other;
                                                        25.78; 64.18;
                                                                      Best Local Similarity 64.1
Matches 881; Conservative
                                                           Query Match
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                                                                                     CAGTAGATTTGAACGAGGCTCCTTTCAAGATAAAAGAGGAGCACTTGAATCGGCTTAGAG 1719
                                                                                                                                                                                             1683 ACAAGATCATGGATGATGA-----AACTGATCCGGTTTCCCTCGGAAGAGACACGTCCG 1736
                                                                                                                                                                                                                       1840 AAGAGCGTCAACTGAAGAAGCAAAGGTACATGGAACTTCAAGAAATTCTGACTAAAGCAT 1899
                                                                                                                                                                                                                                                                                                                                                                                                                                     NIM-1; noninducible immunity; systemic acquired resistance; SAR; pathogen; disease; protection; immunomodulated; plant; cereal; fruit; vegetable; virus; fungi; bacteria; insect; nematode; microbicide; ss.
                                                       GCACTTCTGAGTTCCCACTGGCTAGCATCGGCAAAAAGATGGCTAATGCACAGAGGACAA
                                                                                                                                 CACTCTCTAGAACTGTAGAACTTGGAAAAGGCTTCTTTCCACGTTGTTCAGAAGTTCTAA
                                                                                                                                                                              ATAAGATCATGGATGCTGATGACTTGTCTGAGATAGCTTACATGGGGAATGATACGGCAG
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This sequence encodes a truncated variant NIW-1 protein from Arabidopsis thaliana. This protein is used in a method resulting in the protection of an immunomodulated plant having a first level of resistance and involves treatment with at least 1 microbicide that confers a second level of resistance, such that the plants have a third level of resistance greater than the sum of the first two levels. The method can be applied to a wide variety of plants (cereals, fruits, oilseeds, vegetables etc.) to protect against viruses, fungi, bacteria, insects and nematodes. The method provides a high level of resistance and allows a reduction in the amount of micobicide used. Since the process involves two different methods of protection, it is unlikely that the pathogen will develop resistance to

Sequence 1597 BP; 467 A; 304 C; 381 G; 445 T; 0 other;

ä 1080 CIACAAATGTTGCTAAGAGAGGGCATACTACCCTAGATGCAGATGCATATGT 1139 GTAAAACAAATTACTGATTCACGAGCGGAACTTGGTCTACAAGGGCCTGAAAGCAACGGT 1019 1020 TTTCCTGATAAACATGTTAAGAGGATACATAGGGCATTGGATTCTGATGATGTTGAATTA 1079 GCTGTAGCGTATTGCGATGCAAAGACTACAGCAGAACTTCTAGATCTTGCACTTGCTGAT 1199 ATTAATCATCAAAATTCAAGGGGATACACGGTGCTGCATGTTGCAGCCATGAGGAAAGAG 1259 CCTAAAATTGTAGTGTCCCTTTTAACCAAAGGAGCTAGACCTTCTGATCTGACATCCGAT 1319 GGAAGAAAAGCACTTCAAATCGCCAAGAGGCTCACTAGGCTTGTGGATTTCAGTAAGTCT 1379 GGTAGAACCGCACTCATGATCGCAAAACAAGCCACTATGGCGGTTGAATGTAATATC 771 GTCAAGTTGCTTTTGAAAGAGGATCACAATCTAGATGATGCGTGTGCTCTTCATTTC 531 GAIGIGIGITICGIGIGACAATGACIGCICTCATGIGGCTIGIAGGCCAGCIGIGGCA 719 TICATGITGGAGGITCTCTATITGGCITTCATCTTCAAGAICCCTGAATTAATTACTCTC 183 184 TATCAGAGGCACTTATTGGACGTTGTAGACAAAGTTGTTATAGAGGACACATTGGTTATA 243 CCACAATTGATACTATCTCTATTGGAAAAAGGTGCAAGTGCATCAGAAGCATTTGGAA 4 GATTCGGTTGTGACTGTTTTGGCTTATGTTTACAGCAGCAGCAGTGAGACCGCCGCCTAAA TTATCTGTTGCAAACATTTGTGGTAAAGCATGCGAGAGATTGCTTTCAAGCTGCATTGAG 244 CTCAAGCTTGCTAATATATGTGGTAAAGCTTGTATGAAGCTTGTATGAAGGTTGTAAAAGAG 600 GATGCTGTAATGAGTGTATTGGCTTATTTGTATAGTGGTAAAGTTAGGCCTTCACCTAAA TTCCTGGTTGAGGTTTTGTACACATCATTTACCTTTCAGATCTCTGAATTGGTTGACAAG ATTATTGTCAAGTCTAATGTTGATATCATAACCCTTGATAAAGCCTTGCCTCATGACATT TITCAGAGACACCTACTGGATATICTTGACAAAACTGCAGCAGACGATGTAATGATGGTT DB 19; Length 1597; Indels 0; Mismatches 476; Score 549.4; DB 19 Pred. No. 1.8e-138; 25.3%; Matches 870; Conservative Local Similarity 1380 1200 1260 099 124 780 900 304 096 419 720 64 g g g ò g à g ò qq ö g ò g ò g ά QQ ò ò ò a ò ò ç g

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1857 AAGCAAAGGTACATGGAACTTCAAGAAATTCTGACTAAAGCATTCACTGAGGATAAAGAA 1916
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                                                                                                                                                                                                                                                                                                                                                                                                                                         resistance; mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Non-inducible immunity-1 gene; NIM1 gene; disease resistance; mutan transgenic plant; SAR; systemic acquired resistance; CIM; pathogen; constitutive immunity; agriculture; variant; ss.
                                                                                                                                                        1012 ACTAGCCTCGAGCCTGTCTCACTGGTACGAAGAACATCACCGGGTGTAAAGATA
                                                                                                                                                                                                                                                                         1132 GAACTCGGGAAACGATTCTTCCGGCGCTGTTCGGCAGTGCTCGACCAGATTATGAACTGT
772 CCGGAGCAATGCAAGCATTCTCTCAAAGGCCGACTATGTGTAGAAATACTAGAGCAAGAA
                           GAAAGAAGAGCCCTCTGCTAGGAGAAGCTTCTGTATCTCTTGCTATGGCAGGCGATGAT
                                         TIGCGTATGAAGCTGTTATACCTTGAAAATAGAGTTGGCCTGGCTAAACTCCTTTTTTCCA
                                                                                                                                        1560 ATGGAAGCTAAAGTTGCAATGGACATTGCTCAAGTTGATGGCACTTCTGAGTTCCCACTG
                                                                                                                                                                                                1620 GCTAGCATCG---GCAAAAGATGGCTAATGCACAGAGGACAACAGTAGATTTGAACGAG
                                                                                                                                                                                                                                                      1677 GCTCCTTTCAAGATAAAAGAGGAGCACTTGAATCGGCTTAGAGCACTCTCTAGAACTGTA
                                                                                                                                                                                                                                                                                                                                                                   GATGACTIGICIGAGATAGCTTACATGGGGAATGATACGGCAGAAGAGCGTCAACTGAAG
                                                                                                                                                                                                                                                                                                                                                                                             1192 GAGGACTTGACTCAACTGGCTTGCGGAGAAGACGACACTGCTGAAAACGACTACAAAAG
                                                                                                GAACTTGGAAAACGCTTCTTTCCACGTTGTTCAGAAGTTCTAAATAAGATCATGGATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to wild-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Non-inducible immunity-1 (NIM1) protein variant 2 encoding cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= a
/product= "NIM1 protein variant 2"
/note= "N-terminal deletion compared '
NIM1 sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1312 GAATTAGGAAATTTGTCCCTGACAGATTCGACTTCTTCCAC 1352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1917 GAATATGATAAGACTAACAACATCTCCTCATCTTGTTCCTC 1957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers 1..1410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAV43662 standard; cDNA; 1597
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96US-0033177.
96US-0034379.
96US-0034382.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana.
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27-DEC-1996;
27-DEC-1996;
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This cDNA encodes an altered form of the Arabidopsis thaliana non-
inducible immunity-1 (NIM1) protein. Sequences shown in AAV43661 to
AAV4365 represent variants of the NIM1 cDNA. The invention provides a
chimeric gene comprising a promoter active in plants operatively linked
coll stably transformed with a recombinant vector comprising such a
cells stably transformed with a recombinant vector comprising such a
cells stably transformed with a recombinant vector comprising such a
collineric gene have a broad spectrum of disease resistance. The altered
collineric gene have a broad spectrum of disease resistance. The altered
collineric gene have a broad spectrum of disease resistance (SAR) signal transduction pathway. The transgenic
colliner transformed with an altered NIM1 gene exhibits constitutive SAR
expression which is higher in the transformed plants than in a wild-type
colliner. The products can be used for producing plants with a broad
spectrum disease resistance. Overexpression of NIM1 minics the effects
of inducer compounds that induce constitutive immunity (CIM) phenotype
colliners. The inventions can be used with plants such as rice, wheat,
barley, rye, corn, potato, carrot, sweet potato, sugar beet, bean, pea,
chicory, lettuce, cabbage, cauliflower, broccoli, turnip, radish,
cherry, peach, nectarine, agailic, eggplant, pepper, calery, carrot,
squash, pumpkin, zucchini, cucumber, apple, pear, quince, melon, plum,
cherry, peach, nectarine, apricot, strawberry, grape, raspberry,
conato, sordum and sugarcene. The plants produced are resistant to
a plant pathogens such as virrodes, viroles, fungi, bacteria, insects such,
a suhids and lonidanters and company fungi, bacteria, insects such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ant pathogens such as viruses, viroids, fungi, bacteria, insects such aphids and lepidoptera and nematodes. The plants produced can be used
                                                                                                                                                                                                                                                                                                            Use of non-inducible immunity-1 gene - for transforming plants to produce transgenic plants having a broad spectrum disease resistance
                                                                                                                                                             Steiner HY;
                                                                                                                                                             Ryals JA,
                                                                                                                                                                                                                                                                                                                                                                                     Claim 9; Pages 149-152; 205pp; English.
                                                                                                                                                       Lawton KA,
97US-0034730.
97US-0035021.
97US-0035022.
                                                                                                                                                          Hunt MD,
                                                                                                                                                                                                                                   WPI; 1998-348536/30.
                                                                                                    (NOVS ) NOVARTIS AG
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                                                                                                                                                    Friedrich LB,
                                                   10-JAN-1997;
                           10-JAN-1997;
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Sequence 1597 BP; 467 A; 304 C; 381 G; 445 T; 0 other; Query Match 25.3%; Score 549.4; DB 19; Length 1597; Best Local Similarity 63.9%; Pred. No. 1.8e-138; Matches 870; Conservative 0; Mismatches 476; Indels 15; Ga

2, 243 GATGCTGTAATGAGTGTATTGGCTTATTTGTATAGTGGTAAAGTTAGGCCTTCACCTAAA 659 GAIGIGIGITIGIGIGAGAAAIGACIGCICICAIGIGGCTIGIAGGCCAGCIGIGGCA 719 TICCTGGTTGAGGTTTTGTACACATCATTTACCTTTCAGATCTCTGAATTGGTTGACAAG 779 363 Gaps 63 TATCAGAGGCACTTATTGGACGTTGTAGACAAAGTTGTTATAGAGGACACATTGGTTATA TTATCTGTTGCAAACATTTGTGGTAAAGCATGCGAGAGATTGCTTTCAAGCTGCATTGAG TITCAGAGACACCIACTGGATATICTTGACAAAACTGCAGCAGACGATGTAATGATGGTT ATTATTGTCAAGTCTAATGTTGATATCATAACCCTTGATAAAGCCTTGCCTCATGACATT CTCAAGCTTGCTAATATATGTGGTAAAGCTTGTATGAAGCTATTGGATAGATGTAAAGAG Best Local Similarity 63.9 Matches 870; Conservative 009 4 099 64 720 780 184 840 304 900 ò g ŏ g 셤 g ŏ qq ò δ δý

Search completed: October 7, 2002, 22:58:47

Job time : 253.181 secs

1079 1199 1439 1559 1619 GTAAAAACAAATTACTGATTCACGAGCGGAACTTGGTCTACAAGGGCCTGAAAGCAACGGT 1019 1080 CTACAAATGTTGCTAAGAGGGGCATACTACCTAGATGATGCATATGCTCTCCATTAT 1139 GGAAGAAAAGCACTTCAAATCGCCAAGAGGCTCACTAGGCTTGTGGATTTCAGTAAGTCT 1379 GAAAGAAGAAGCCTCTGCTAGGAGAAGCTTCTGTATCTTTGCTATGGCAGGCGATGAT 1499 1620 GCTAGCATCG---GCAAAAAGATGGCTAATGCACAGAGGACAACAGTAGATTTGAACGAG 1676 AAGCAAAGGTACATGGAACTTCAAGAAATTCTGACTAAAGCATTCACTGAGGATAAAGAA 1916 1192 GAGGACTTGACTCAACTGGCTTGCGGAGAAGACGACACTGCTGAGAAACGACTACAAAAG 1251 AAGCAAAGGTACATGGAAATACAAGAGACACTAAAGAAGGCCTTTAGTGAGGACAATTTG 1311 471 651 831 951 -----AGAAACATGTCTCGAATGTACATAAGGCACTTGACTCGGATGATATTGAGTTA GCTGTAGCGTATTGCGATGCAAAGACTACAGCAGAACTTCTAGATCTTGCACTTGCTGAT 1200 ATTAATCATCAAAATTCAAGGGGATACACGGTGCTGCATGTTGCAGCCATGAGGAAAGAG GATGACTTGTCTGAGATAGCTTACATGGGGAATGATACGGCAGAGAGGCGTCAACTGAAG 592 GTCAACCATAGGAATCCGAGGGGATATACGGTGCTTCATGTTGCTGCGATGCGGAAGGAG CCTAAAAATTGTAGTGCCCTTTTAACCAAAGGAGCTAGACCTTCTGATCTGACATCCGAT GCTCCTTTCAAGATAAAAGAGGAGCACTTGAATCGGCTTAGAGCACTCTCTAGAACTGTA .020 TTTCCTGATAAACATGTTAAGAGGATACATAGGGCATTGGATTCTGATGATGTTGAATTA GGTAGAACCGCACTCATGATCGCAAAACAAGCCACTATGGCGGTTGAATGTAATATC GACAAACGAGAACAAATTCCTAGAGATGTTCCTCCTCTTTTGCAGTGGCGGCCGATGAA TTGCGTATGAAGCTGTTATACCTTGAAAATAGAGTTGGCCTGGCTAAACTCCTTTTTTCCA ATGGAAGCTAAAAGTTGCAATGGACATTGCTCAAGTTGATGGCACTTCTGAGTTCCCACTG GAACTTGGAAAACGCTTCTTTCCACGTTGTTCAGAAGTTCTAAATAAGATCATGGATGCT GAATATGATAAGACTAACATCTCCTCATCTTGTTCCTC 1957 1140 1260 832 1320 712 1380 1440 1500 1560 952 1677 1072 1737 1797 1857 1252 1917 1132 qq ò pp QΥ qq Qγ δ qq QY g ò g ŏ g δ g ŏ ρp ò g δ g q qq q δ ò ò

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Sequence 220, I
Sequence 2, Apl
Sequence 3, Apl
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6: /cgn2_6/ptcdata/2/lna/PCTUS_COMB.seg:*
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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Sequence 595, App Sequence 389, App Sequence 4, Appli Sequence 7, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 1, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 27, Appli Sequence 4, Appli	CONFERRING			
28 36.4 1.7 658 4 US-08-998-416-595 29 36.2 1.7 613 4 US-09-328-111-389 30 36.2 1.7 613 4 US-09-328-111-389 31 35.8 1.6 161 4 US-08-952-061-4 32 35.8 1.6 1364 2 US-08-623-06A-7 35.4 1.6 1364 1 US-08-621-493-3 35.4 1.6 1364 2 US-08-955-087-3 36 35.4 1.6 1364 2 US-08-965-688-3 37 35.2 1.6 2274 3 US-08-965-68-3 39 35.2 1.6 2274 3 US-08-423-752-13 41 35.2 1.6 2274 4 US-09-16-873-27 42 35.2 1.6 2274 4 US-09-366-431-27 43 35 1.6 1815 4 US-09-366-935-2 44 34.6 1.6 2248 3 US-09-366-935-2 44 34.6 1.6 2248 4 US-09-141-047-7 45 34.2 1.6 2248 3 US-09-141-047-7	ESULT 1 (S-08-989-478-6 Sequence 6, Application US/08989478 Patent No. 5986082 GENERAL INFORMATION: APPLICANT: Uknes, Scott APPLICANT: Uknes, Scott APPLICANT: Steiner, Henry-York APPLICANT: Steiner, Henry-York APPLICANT: Ryals, John TITLE OF INVENTION: ALTERED FORMS OF THE NIMI GENE	NUMBER OF SEQUENCES: 32 CORRESPONDENCE ADDRESS: 32 CORRESSEE: No. 5986082arti STREET: 3054 Cornwallis Ro CITY: Research Trianglis Ro CITY: No. 5986082th Carol COUNTRY: No. 5986082th Carol COUNTRY: No. 5986082th Carol COUNTRY: ISA ZIP: 27709 COMPUTER: READABLE FORM: COMPUTER: IBM FC compatibl OPERATING SYSTEM: PC-DOS/M SOFTWARE: Patentin Release	5/08/989,478 60/033,177 996 5 60/034,379 5 60/034,382 5 60/034,382	•

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CYHER INFORMATION: /product- "NIMI protein"
US-08-989-478-6
                                                                                      TOPOLOGY: linear
ONGLECULE TYPE: CDNA
ONIGINAL SOURCE:
ORGANISM: Arabidopsis thaliana
       TELEPHONE: (919) 541-8689
INFORMATION FOR SEO ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 2011 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TELECOMMUNICATION INFORMATION: TELEPHONE: (919) 541-8587
                                                                                                                                             NAME/KEY: misc_feature
LOCATION: 1..2011
OTHER INFORMATION: /note=
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Best Local Similarity 62.7%
Matches 981; Conservative
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Patent No. 5986082
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Uknes, Scott
APPLICANT: Hunt, Michelle
APPLICANT: Steiner, Henry-York
APPLICANT: Ryals, John
TITLE OF INVENTION: ALTERED FORMS OF THE NIM1 GENE CONFERRING
TITLE OF INVENTION: DISEASE RESISTANCE IN PLANTS
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                                                                  335 CTAAGAAGGAGAAAGACTCCAACAACACCGCCGCCGTGAAGCTCGAGCTTAAGGAGATTG 394
                                                                                                                    535 AAAAGGAGAAATAGTAGT-------AAGGTGGAATTGAAGGAGGTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product= "altered form of NIM1" // Note= "Serine residues at amino acid positions 55 and 59 wild-type NIM1 gene product have been changed to Alanine residues "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "nucleotides 205 and 217 changed from T's to G's compared to wild-type sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    415 CGGAGTTTGACTACTTCGCCGACGCTAAGCTTGTGGTTTCCGGCCCGTGTAAGGAAATTC 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGGTGCACCGGTGCATTTTGTCGGCGAGGAGTCCGTTCTTTAAGAATTTGTTCTGCGGTA 534
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26.6%; Score 576.8; DB 2; Length 2011; 62.7%; Pred. No. 1.5e-155;
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                              No. 5986082artis Corporation
                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 60/034,379
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,382
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 60/034,730 FILING DATE: 10-JAN-1997 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 60/035,021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,022
FILING DATE: 10-JAN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/989,478
                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 60/033,177 FILING DATE: 13-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UMBER: US 60/035,021
10-JAN-1997
                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                              : 3054 Cornwallis Road
Research Triangle Park
No. 5986082th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF.
TELECOMMUNICATION INFORMATION:
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OTHER INFORMATION: residu
FEATURE:
NAME/KEY: misc_feature
LOCATION: 205.217
OTHER INFORMATION: /note
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EDNESS: single
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PRIOR APPLICATION DATA:
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               CORRESPONDENCE ADDRESS:
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OTHER INFORMATION:
SEOUENCES:
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                                                                                                                                                                                                                                               FILING DATE:
                                  ADDRESSEE:
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981;
                                                                                             COUNTRY:
                                              STREET:
CITY: Re
STATE: 1
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Matches
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1653
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1597 ATGGCACTTCTGAGTTCCCACTGGCTAGCATCG---GCAAAAAGATGGCTAATGCACAGA
                                                                                  1714 TTAGAGCACTCTCTAGAACTGTAGAACTTGGAAACGCTTCTTCCACGTTGTTCAGAAG
                                                                                                                                            1523 TAAAAGCGCTTTCTAAAACCGTGGAACTCGGGAAACGATTCTTCCCGGCGCTGTTCGGCAG
                              1403 AGGGAACATGTGAGTTCATAGTGACTAGCCTCGAGCCTGACCGTCTCACTGGTACGAAGA
                                                                                                                                                                                                                                                         CGGCAGAAGAGCGTCAACTGAAGAAGCAAAGGTACATGGAACTTCAAGAAATTCTGACTA
                                                               GGACAACAGTAGATTTGAACGAGGCTCCTTTCAAGATAAAAGAGGAGCACTTGAATCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Kessmann, Helmut
APPLICANT: Oostendorp, Michael
TITLE OF INVENTION: METHOD FOR PROTECTING PLANTS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: No. 6031153artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6031153th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,379
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,382
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APPLICATION NUMBER: US 08/761,543
FILING DATE: 6-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,378
FILING DATE: 27-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Friedrich, Leslie
Uknes, Scott
Molina, Antonio
Ruess, Wilhelm
Knauf-Beiter, Gertrude
Kung, Ruth
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/08996685
Patent No. 6031153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ryals, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Ryals,
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                                                                                                                                                                                                                                                                                                                                                                                      CCTC 1957
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  275 CTITCCACCGGTGCGTTTTGTCAGCGAGAAGCTCTTTCTTCAAGAGCGCTTTAGCCGCCG 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  335 CTAAGAAGGAGAAAAGACTCCAACAACACGCCGCCGTGAAGCTCGAGCTTAAGGAGATTG 394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "NIM1 cDNA sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 576.8; DB 3;
Pred. No. 1.5e-155;
0; Mismatches 547;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product= "NIM1 protein'
               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,730
FILING DATE: 10-UAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,021
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,022
FILING DATE: 10-JAN-1997
                                                                                                                                                                                    FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,024
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/875,015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                               FILING DATE: 16-105-20707

ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5
TELECOMMUNICATION INFORMATION:
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ilarity 62.7%;
Conservative 0
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FILING DATE: 27-DEC-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 2011 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: 1..2011
OTHER INFORMATION: /not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION: 43.1824
; OTHER INFORMATION:
US-08-996-685-6
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ORIGINAL SOURCE:
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Matches 981;
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                                                                                                                                                                                                                                                                                                                          TTCTAGATCTTGCACTTGCTGATATTAATCATCAAAATTCAAGGGGATACACGGTGCTGC 1236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCCITGTGGATTICAGIAAGTCTCCGGAGGAAAATCTGCTTCGAATGATCGTTAT 1416
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                       937 ATAAAGCCTTGCCTCATGACATTGTAAAACAAATTACTGATTCACGAGCGGAACTTGGTC 996
                                                                                                                                       AAAAGTCATTGCCGGAAGAGCTTGTTAAAGAGATAATTGATAGACGTAAAGAGCTTGGTT 814
        817 CAGCAGACGATGTAATGATGGTTTTATCTGTTGCAAACATTTGTGGTAAAGCATGCGAGA
                                                            GATTGCTTTCAAGCTGCATTGAGATTATTGTCAAGTCTAATGTTGATATCATAACCCTTG
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1894 AAGCATTCACTGAGGATAAAGAAGAATATGATAAGACTAACAACATCTCCTCATCTTGTT 1953
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TITLE OF INVENTION: METHOD FOR PROTECTING PLANTS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38,241
ER: PF/5-21215/P1/CGC1912
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEE: No. 6031153artis Corporation
: 3054 Cornwallis Road
Research Triangle Park
No. 6031153th Carolina
Y: USA
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/761,543
FILING DATE: 6-DEC-1996
PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,021
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FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 60/034,730
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10-JAN-1997
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10-JAN-1997
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                                                                                                                                                                                                                                             Ryals, John
Friedrich, Leslie
Uknes, Scott
Molina, Antonio
Ruess, Wilhelm
Knauf-Beiter, Gertrude
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                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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                                                                                                                                                                                                                                                                                                                                                      Kung, Ruth
Kessmann, Helmut
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Meigs, J. Timothy REGISTRATION NUMBER: 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 27709
COMPUTER READABLE FORM:
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STREET: 30
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APPLICANT:
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                                                                                                                                                                     US-08-996-885-7
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STATE:
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ATGTTGCAGCCATGAGGAAAGAGCCTAAAATTGTAGTGTCCCTTTTAACCAAAGGAGCTA 1296
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863 ITGACTCGGATGATATTGAGTTAGTCAAGTTGCTTTTGAAAGAGGATCACACCAATCTAG
                                                             TICTAGATCTIGCACTIGCTGATATTAATCATCAAAATTCAAGGGGATACACGGTGCTGC
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Patent No. 5986082
GENERAL INFORMATION:
APPLICANT: Unkes, Scott
APPLICANT: Hunt, Michelle
APPLICANT: Steiner, Henry-York
APPLICANT: Ryals, John
TITLE OF INVENTION: ALTERED FORMS
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US-08-989-478-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                to wild-type sequence."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                 MAME/KEY: CDS
LOCATION: 43..1824
COCHER INFORMATION: //OCE= "Serine residues at amino acid OTHER INFORMATION: wild type NIMI gene product have been OTHER INFORMATION: wild type NIMI gene product have been OTHER INFORMATION: residues."

FEATURE:
NAME/KEY: misc_feature
LOCATION: 205..217
OTHER INFORMATION: Coche "nucleotides 205 and 217
OTHER INFORMATION: changed from T's to G's compared to vocate the compared t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. Similarity 62.7%; Pred. No. 1.5e-155; Conservative 0; Mismatches 547;
               TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2011 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
    (919) 541-8587
                                                                                                                                                                        MOLECULE TYPE: CDNA
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hes 981;
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Matches
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                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/989,478 FILING DATE:
CLASSIFICATION:
DISEASE RESISTANCE IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PF/5-21214/P1/CGC1911
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                                    SSEE: No. 5986082artis Corporation Cornwallis Road Cornwallis Road Research Triangle Park No. 5986082th Carolina
                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 60/034,730 FILING DATE: 10-JAN-1997
                                                                                                                                                                                                                                                                                                          US 60/034,379
                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 60/033,177
FILING DATE: 13-DEC-1996
                                                                                                                                                                                                                                                                                                                                                     us 60/034,382
                                                                                                                                                                                                                                                                                                                                                                                                                                      US 60/035,021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               us 60/035,022
                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: PF/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEPAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Meigs, J. Timothy REGISTRATION NUMBER: 38,241
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60
DITING DATE: 27-DEC-1996
                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 60 FILING DATE: 27-DEC-1996 KIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60
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ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1597 base pairs
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
                                                                                                           ZIP: 27709
COMPUTER READABLE FORM:
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           OF SEQUENCES:
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LOCATION: 1..1
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                                                                                               USA
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                                       ADDRESSEE:
STREET: 30
                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-989-478-9
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TITCAGAGACACCTACTGGATATTCTTGACAAAACTGCAGCAGACGATGTAATGATGGTT
                                                                                             244 CTCAAGCTTGCTAATATATGTGGTAAAGCTTGTATGAAGCTATTGGATGTAAAGAG
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                                                                       TTATCTGTTGCAAACATTTGTGGTAAAGCATGCGAGAGATTGCTTTCAAGCTGCATTGAG
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1857 AAGCAAAGGTACATGGAACTTCAAGAAATTCTGACTAAAGCATTCACTGAGGATAAAGAA 1916
                             1252 AAGCAAAGGTACATGGAAATACAAGAGACACTAAAGAAGGCCTTTAGTGAGACAATTG 1311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1917 GAATATGATAAGACTAACAACATCTCCTCATCTTGTTCCTC 1957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Oostendorp, Michael
TITLE OF INVENTION: METHOD FOR PROTECTING PLANTS
NUMBER OF SEQUENCES: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: PF/5-21215/P1/CGC1912 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 3054 Cornwalls Road CITY: Research Triangle Park STRTE: No. 6031153th Carolina COUNTR: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/761,543
FILING DATE: 6-DEC-1996
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICA
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APPLICATION NUMBER: US 60/034,382
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 60/034,730
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
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FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,022
FILING DATE: 10-JAN-1997
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APPLICATION NUMBER: US 60/035,024
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/875,015
FILING DATE: 16-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA: US/08/996,685 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                      Ryals, John
Friedrich, Leslie
Uknes, Scott
Molina, Antonio
Ruess, Wilhelm
Knauf-Beiter, Gertrude
Kung, Ruth
                                                                                                                                                                                                                                                                                                        Sequence 9, Application US/08996685 Patent No. 6031153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kessmann, Helmut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Ryals,
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APPLICANT:
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/product= "Altered form of NIM1"
/note= "N-terminal deletion compared to wild-type NIM1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTAAAACAAATTACTGATTCACGAGCGGAACTTGGTCTACAAGGGCCTGAAAGCAACGGT 1019
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTATTGTCAAGTCTAATGTTGATATCATAACCCTTGATAAAGCCTTGCCTCATGACATT 959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    532 GCTGTTGCATATTGCAATGTGAAGACCGCAACAGATCTTTTAAAAACTTGATCTTGCCGAT 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            660 GATGTGTGTTTGTGTGGACAATGACTGCTCTATGTGGGCTTGTAGGCCAGCTGTGGCA 719
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTTCAGAGACACCTACTGGATATTCTTGACAAAACTGCAGCAGGACGATGTAATGATGGTT 839
                                                                                                                                                                                                                                                                                                                                                                                                                                           600 GATGCTGTAATGAGTGTATTGGCTTATTTGTATAGTGGTAAAGTTAGGCCTTCACCTAAA 659
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Pred. No. 9.6e-148;
0; Mismatches 476;
                                                                                                                                                                                                                                                                                                  sednence.
TELEPHONE: (919) 541-8587
TELERAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1597 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                            25.3%;
                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                               OTHER INFORMATION:
US-08-996-685-9
                                                                                                                                                                                                                                  LOCATION: 1..1410
OTHER INFORMATION:
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1440 GAAAGAAGACCCTCTGCTAGGAGAAGCTTCTGTATCTCTTTGCTATGGCAGGGGATGAT 1499
                                                                                                                                                           ATGGAAGCTAAAAGTTGCAAATGGACATTGCTCAAGTTGATGGCACTTCTGAGTTCCCACTG 1619
                                                                                                                                                                              1620 GCTAGCATCG----GCAAAAGATGGCTAATGCACAGAGGACAACAGTAGATTTGAACGAG 1676
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                                                                                                                                                                                                                                                                                    GATGACTTGTCTGAGATAGCTTACATGGGGAATGATACGGCAGAAGAGGGGTCAACTGAAG 1856
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                                                                                                                                                                                                                                                                                                                                                                                              AAGCAAAGGTACATGGAACTTCAAGAAATTCTGACTAAAGCATTCACTGAGGATAAAGAA
                                                                                                          TIGCGTATGAAGCTGTTATACCTTGAAAATAGAGTTGGCCTGGCTAAACTCCTTTTTCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Uknes, Scott
APPLICANT: Hunt, Michelle
APPLICANT: Hunt, Michelle
APPLICANT: Steiner, Henry-York
APPLICANT: Ryals, John
TITLE OF INVENTION: ALTERED FORMS OF THE NIM1 GENE CONFERRING
TITLE OF INVENTION: DISEASE RESISTANCE IN PLANTS
NUMBER OF SEQUENCES: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1917 GAATATGATAAGACTAACAACATCTCCTCCTCTTGTTCCTC 1957
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/989,478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSE: No. 5986082artis Corporation
STREET: 3054 Cormwallis Road
CITY: Research Triangle Park
STATE: No. 5986082th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,177
FILING DATE: 13-DEC-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 11, Application US/08989478 Patent No. 5986082 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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ADDRESSEE: No. 59860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
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/product= "Altered form of NIM1" /note= "C-terminal deletion compared to wild-type NIM1."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                335 CTAAGAAGGAGAAAAACTCCAACAACACCGCCGCGTGAAGCTCGAGCTTAAGGAGATTG 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGGCTTGTAGGCCAGCTGTGGCATTCCTGGTTGAGGTTTTGTACACATCATTACCTTTC 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAGCAGACGATGTAATGATGGTTTTATCTGTTGCAAACATTTGTGGTAAAGCATGCGAGA 876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           275 CITTCCACCGGGGGGTTTTGTCACGAGAAGCTCTTTCTTCAAGAGGGCTTTAGCGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      577 IGAAAGAGCAIGAGGIGAGCIAIGAIGCIGIAAIGAGIGIAIIGGCIIAIITGIAIAGIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              218 CGCCGGATGATTTCTACAGCGACGCTAAGCTTGTTCTCTCCGAC---GGCCGGGAAGTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             877 GATTGCTTTCAAGCTGCATTGAGATTATTGTCAAGTCTAATGTTGATATCATAACCCTTG
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                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: PF/5-21214/P1/CGC1911
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 517.4; DB 2;
Pred. No. 1.5e-138;
0; Mismatches 481;
                                                                                                                                 FILING DATE: 10-10AN-1997
FILING DATE: 10-10AN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,021
FILING DATE: 10-1AN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,022
FILING DATE: 10-1AN-1997
ATTORNEY/AGENT INFORMATION:
                                              FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,382
FILING NAME
  US 60/034,379
                                                                                                                                                                                                                                                                                                    NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 23.8%;
Best Local Similarity 63.0%;
Matches 882; Conservative
                       27-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 1608 base pairs
nucleic acid
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; OTHER INFORMATION: /E
; CHER INFORMATION: /n.
                FILING DATE: 27-DEC-1
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
LOCATION:
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Knauf-Beiter, Gertrude Kung, Ruth Kessmann, Helmut

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APPLICANT: Kung, Ruth
APPLICANT: Kessmann, Helmut
APPLICANT: Oostendorp, Michael
TITLE OF INVENTION: METHOD FOR PROTECTING PLANTS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                   AUDRESSEE: No. 6031153artis Corporation STREET: 3054 CORMANIIS Road CITY: Research Triangle Park STATE: No. 60311531
                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/761,543
FILING DATE: 6-DEC-1996
                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/996,685
                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: '(FILING DATE: 27-DEC-1
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APPLICATION NUMBER: I
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                                                                                             TACAAGGGCCTGAAAGCAACGGTTTTCCTGATAAACATGTTAAGAGGATACATAGGGCAT 1056
                                                                                                                                                                                                                            ATGATGCATATGCTCTCCATTATGCTGTAGCGTATTGCGATGCAAAGACTACAGCAGAAC 1176
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                                                                                                                                                             TGGATTCTGATGATGTTGAATTACTACAAATGTTGCTAAGAGAGGGGGCATACTACCCTAG 1116
                                                                                                               695 AGCTATTGGATAGATGTAAAGAGATTATTGTCAAGTCTAATGTAGATATGGTTAGTCTTG 754
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                                                              755 AAAAGTCATTGCCGGAAGAGCTTGTTAAAGAGATAATTGATAGACGTAAAAGAGCTTGGTT
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JMBER: US 60/034,379 27-DEC-1996

UMBER: 'US 60/034,378 27-DEC-1996

Version #1.30

PC-DOS/MS-DOS

MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-

FILING DATE:

No. 6031153th Carolina: USA

27709

COUNTRY:

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LOCATION: 43.1608
CTHER INFORMATION: /product= "Altered form of NIM1"
CTHER INFORMATION: /note= "C-terminal deletion compared to wild-type NIM1."
US-08-996-685-11
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Pred. No. 1.5e-138;
0; Mismatches 481;
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,382
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,730
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATE: US 60/035,021
FILING DATE: 10-JAN-1997
                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,022
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,024
                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US_08/875,015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Meigs, J. Timothy REGISTRATION NUMBER: 38,241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23.8%;
                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 16-JUL-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                         FILING DATE: 10-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1608 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: CDNA
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Matches 882; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
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Sequence 11, Application US/08996685
Patent No. 6031153
GENERAL INFORMATION:
APPLICANT: Ryals, John
APPLICANT: Friedrich, Leslie
APPLICANT: Whees, Scott
APPLICANT: Molina, Antonio
APPLICANT: Ruess, Wilhelm

US-08-996-685-11

us-08-908-884-13.rni

Oy Dp	OY 415 CGGAGTTTGACTACGCCGACGCTAAGCTTGTGGTTTCCGGCCCGTGTAAGGAATTC	TTCCGCCCCTGTAAGGAAATTC 474
QY	QY 475 CGGTGCACCGGTGCATTTTGTCGGCGAGGAGTCCGTTCTTTAAGAATTTGTTCTGCGGTA	CTTTAAGAATTTGTTCTGCGGTA 534
Qy Db	535 AAAAGGAGAAGAATAGTAGT	AAGGIGGAATIGAAGGAGTGA 576 
Qy Dp	QY 577 TGAAAGAGCATGAGGTGAGGTGTGTAATGAGTGTATTGGCTTATTGTATAGTGTGTATGTGTATAGTGTATAGTAGTGTATAGTAG	TGTATTGGTTATTGTATAGTG 636 
Qy Db	637	TGTGGACAATGACTGCTCATG 696
oy Db	QY 697 TGGCTTGTAGGCCAGCTGTGGCATTCCTGGTTGAGGTTTTGTACACATCATTACCTTTC	TTTGTACACATCATTACCTTC 756
Oy Dp	OY 757 AGATCTCTGAATTGGTTGACAAGTTTCAGAGACACCTACTGGATATTCTTGACAAAACTG	ACTGGATATTCTTGACAAAACTG 816                           ATTGGACGTTGTAGACAAAGTTG 634
Qy Db	817 CAGCAGACGATGTAATGATGGTTTTATCTGTTGCAAACATT	CATTTGTGGTAAAGCATGCGAGA 876 
Qy	OY 877 GATIGCITICAAGCIGCATIGAGAITATIGICAAGICIAAIGTIGAIGAICATAACCCTIG	TAATGTTGATATCATAACCCTTG 936 
Qy	QY 937 ATAAAGCCTTGCCTCATGACATTGTAAAACAAATTACTGATTCACGAGCGGAACTTGGTC	TGATTCACGAGCGGAACTTGGTC 996
Qy	OY 997 TACAAGGCCTGAAAGCAACGGTTTTCCTGATAAACATGTTAAGAGGATACATAGGGCAT	TGTTAAGAGGATACATAGGCAT 1056 
07 D	1057	AAGAGAGGGCATACTACCCTAG 1116 
Qy Db	OY 1117 ATGATGCATATGCTCTCCATTATGCTGTAGCGTATTGCGATGCAAGACTACAGCAGAACC	CGATGCAAAGACTACAGCAGAAC 1176 
Qy	OY 1177 TICTAGATCTIGCACTIGCIGAIATTAATCATCAAAATTCAAGGGGATACACGGTGCTGC D 983 TITTAAAACTIGATCTIGCCGATGTCAACCAIAGGAATCCGAGGGGATATACGGTGCTTC	TTCAAGGGGATACACGGTGCTGC 1236 
Oy Dp	OY 1237 ATGTTGCAGCCATGAGGAAGAGCCTAAAATTGTAGTGTCCCTTTTAACCAAAGGAGCTA 	GTCCCTTTTAACCAAAGGAGCTA 1296 
Oy Dp	OY 1297 GACCTTCTGATCTGACATCCGATGGAAGAAAGCACTTCAAATCGCCAAGAGGCTCACTA	TCAAATCGCCAAGAGGCTCACTA 1356            CATGATCGCAAAACAAGCACTA 1162
Qy Db	OY 1357 GGCTTGTGGATTTCAGTAAGTCTCCGGAGGAAGGAAAATCTGCTTCGAATGATCGGTTAT	ATCTGCTTCGAATGGTCGGTTAT 1416
Oy Dp	OY 1417 GCATTGAGAATCTGGAGCAAGCAGAAAGAAGAGCCTCTGCTAGGAGAAGCTTCTGTAT 	ICTGCTAGGAGAAGCTTCTGTAT 1476

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1537 GCCIGGCTAAACTCCTTTTTCCAATGGAAGCTAAAGTIGCAATGGCTCAAGTIG 1596
                                                                                                                                                            CTCTTGCTATGGCAGGCGATGATTTGCGTATGAAGCTGTTATACCTTGAAAATAGAGTTG 1536
                  GGACAACAGTAGATTTGAACGAGGCTCCTTTCAAGATAAAAGGGGGGGCACTTGAATCGGC 1713
                                                                                                                                                                                                                                   TTAGAGCACTCTCTAGAACTGTAGAACTTGGAAAACGCTTCTTTCCACGTTGTTCAGAAG 1773
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APPLICANT: UKnes, Scott
APPLICANT: Uknes, Scott
APPLICANT: Uknes, Scott
APPLICANT: Steiner, Henry-York
APPLICANT: Steiner, Henry-York
TITLE OF INVENTION: ALTERED FORMS OF THE NIMI GENE CONFERRING
TITLE OF INVENTION: DISEASE RESISTANCE IN PLANTS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/989,478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: No. 5986082artis Corporation STREET: 3054 Cornwallis Road CITY: Research Triangle Park STATE: No. 5986082th Carolina COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 60/033,177
FILING DATE: 13-DEC-1966
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 60/034,379
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 60/034,382
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 60/034,730
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUBER: US 60/035,021
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUBER: US 60/035, 021
FILING DATE: 10-JAN-1997
ATTORNEY AGENT INFORMATION:
NAME: Meigs, J. Timothy
                                                                                                                                                                                                                                                                                                                                                                                                                                      1774 TTCTAAATAAGATCATGGA 1792
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COMPUTER READABLE FORM:
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COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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                                                                                                                                                                                                                                                                                                                                                                          600 GATGCTGTAATGAGTGTATTGGCTTATTTGTATAGTGGTAAAGTTAGGCCTTCACCTAAA 659
                                                                                                                                                                                                                                                                                                                                                                                                                                         GATGTGTGTGTTTGTGTGGACAATGACTGCTCTCATGTGGCCTTGTAGGCCAGCTGTGGCA 719
                                                                                                                                                                                                                                                                                                          Query Match 22.6%; Score 490; DB 2; Length 1194; Best Local Similarity 64.5%; Pred. No. 8.8e-131; Matches 771; Conservative 0; Mismatches 410; Indels 15; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                         4 GATTCGGTTGTGACTGTTTTGGCTTATGTTTACAGCAGCAGAGTGAGACCGCCGCCTAAA 63
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/note= "N-terminal/C-terminal chimera."
                    75-21214/P1/CGC1911
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REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8689
INFORMATION FOR SED ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1194 base pairs
TYPE: nuclet acid
STRANDEDNESS: single
TOPOLOGY: Linear
MOLECULE TYPE: CDNA
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CTHER INFORMATION:
CTHER INFORMATION:
US-08-989-478-13
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ATGGAAGCTAAAAGTTGCAATGGACATTGCTCAAGTTGATGGCACTTCTGAGTTCCCACTG 1619
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                                                   GAAAGAAGAACCCTCTGCTAGGAGAAGCTTCTGTATCTCTTGCTATGGCAGGCGATGAT 1499
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                                                                                                    772 CCGGAGCAATGCAAGCATTCTCTCAAAGGCCGACTATGTGTAGAAATACTAGAGCAAGAA 831
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                                                                                                                                                                                                                                                               TIGCGTATGAAGCTGTTATACCTTGAAAATAGAGTTGGCCTGGCTAAACTCCTTTTTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Oostendorp, Michael TITLE OF INVENTION: METHOD FOR PROTECTING PLANTS NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: No. 6031153artis Corporation
STREET: 3054 Cormuallis Road
CITY: Research Triangle Park
STATE: No. 6031153th Carolina
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APPLICATION UNBER: US 08/761,543
FILING DATE: 6-DEC-1996
PRIOR APPLICATION UNBER: US 60/034,378
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
FILING DATE: 27-DEC-1996
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Ryals, John
APPLICANT: Friedrich, Leslie
APPLICANT: Uknes, Scott
APPLICANT: Wolina, Antonio
APPLICANT: Ruess, Wilhelm
APPLICANT: Knauf-Beiter, Gertrude
APPLICANT: Knauf-Beiter, Gertrude
APPLICANT: Knsuf-Beiter, Helmut
APPLICANT: Costendorn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0,
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; Patent No. 6031153
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1080 CTACAAATGTTGCTAAGAGAGGGGCATACTACCCTAGATGATGCATATGCTCTCCATTAT 1139
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STREET: 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 490; DB 3; Length 11
Pred. No. 8.8e-131;
0; Mismatches 410; Indels
                                                                                                                                                                                                                                                NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-21215/P1/CGC1912
TELECOMNUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEPHONE: (919) 541-8689
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                     APPLICATION NUMBER: US 08/875,015 FILING DATE: 16-JUL-1997 ATTORNEY/ABENT INFORMATION:
                                                                                             FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,022
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,024
                                            APPLICATION NUMBER: US 60/034,730
                                                                                     us 60/035,021
                                                                                                                                                                  JMBER: US 60/035,024
10-JAN-1997
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64.5%;
AND DATE: 27-DEC-1996
PRIOR APPLICATION NIMES APPLICATION NIMES EDITOR
                                                   FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60
                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1194 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 22.6
Best Local Similarity 64.5
Matches 771; Conservative
                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid STRANDEDNESS: single
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
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GCTGTAGCGTATTGCGATGCAAAGACTACAGCAGAACTTCTAGATCTTGCACTTGCTGAT 1199
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                                                                                                                                                                                                                                                                                     CCTAAAATTGTAGTGTCCCTTTTAACCAAAGGAGCTAGACCTTCTGATCTGACATCCGAT 1319
                                                                                                                                                                                                                                                                                                                                                                                         GGAAGAAAAGCACTTCAAATCGCCAAGAGGCTCACTAGGCTTGTGGATTTCAGTAAGTCT 1379
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472 GTCAAGTTGCTTTTGAAAGAGATCACACCAATCTAGATGCGTGTGCTCTTCATTTC 531
                                                                                                                                                                                                              592 GTCAACCATAGGAATCCGAGGGGATATACGGTGCTTCATGTTGCTGCCATGCGGAAGGAG 651
                                                                                                                                                                                                                                                                                                                1737 GAACTIGGAAAACGCTTCTTTCCACGTTGTTCAGAAGTTCTAAATAAGATCATGGA 1792
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APPLICANT: Hunt, Michelle
APPLICANT: Hunt, Michelle
APPLICANT: Hunt, Michelle
APPLICANT: Ryals, John
TITLE OF INVENTION: ALTERED FORMS OF THE NIMI GENE CONFERRING
TITLE OF INVENTION: DISEASE RESISTANCE IN PLANTS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: No. 5986082artis Corporation
STREET: 3054 Cormwallis Road
CITY: Research Triangle Park
STATE: No. 5986082th Carolina
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1158 GCAAAGACTACAGCAGAACTTCTAGATCTTGCACTTGCTGATATTAATCATCAAAATTCA 1217
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LOCATION: 4271..4474
OTHER INFORMATION: /product= "3rd exon of NIM1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 4586..4866
OTHER INFORMATION: /product= "4th exon of NIM1"
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    PatentIn Release #1.0, Version #1.30
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0; Mismatches 392;
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Pred. No. 1.3
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                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,177
FILING DATE: 13-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,379
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,382
FILING DATE: 27-DEC-1996
                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,021
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,022
FILING DATE: 10-JAN-1997
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 3427..4162
OTHER INFORMATION: /product= "2nd
                                                                                                                                                                                                                      PELING APPLICATION DATA:
APPLICATION NUMBER: US 60/034,730
FILING DATE: 10-JAN-1997
                                  US/08/989,478
                                                                                                                                                                                                                                                                                                                                                                                                          38,241
                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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58.6%;
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                          J. Timothy
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Matches 714; Conservative
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                                  APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
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LOCATION: 2787.
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HYPOTHETICAL: NO
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; LOCATION:
US-08-989-478-1
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APPLICANT: Kung, Ruth
APPLICANT: Kessmann, Helmut
APPLICANT: Oostendorp, Michael
TITLE OF INVENTION: METHOD FOR PROTECTING PLANTS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF/5-21215/P1/CGC1912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: No. 6031153artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6031153th Carolina
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRICR APPLICATION DATA:
APPLICATION NUMBER: US 08/761,543
FILING DATE: 6-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,378
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,379
FILING DATE: 27-DEC-1996
PRIOR APPLICATION NUMBER: US 60/034,382
FILING DATE: 27-DEC-1996
PRIOR APPLICATION NUMBER: US 60/034,382
FILING DATE: 27-DEC-1996
PRIOR APPLICATION NUMBER: US 60/034,382
FILING DATE: 27-DEC-1996
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FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,022
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,024
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,024
FILING DATE: 10-JAN-1997
                                                                                                                                                                                       Ryals, John
Friedrich, Leslie
Uknes, Scott
Molina, Antonio
Ruess, Wilhelm
Knauf-Beiter, Gertrude
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FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/875,015
FILING DATE: 16-JUL-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                  Sequence 1, Application US/08996685 Patent No. 6031153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Melgs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INPORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
                                                                                                                                                                   GENERAL INFORMATION:
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APPLICANT:
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                                                                  RESULT 12
US-08-996-685-1
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join(2787..3347, 3427..4162, 4271..4474, 4586..4866)
                                                                                                                                                                                                                                                                                                                                                 Length 5655;
                                                                                                                                                                                      NAME/KEY: exon
LOCATION: 4271..4474
OTHER INFORMATION: /product= "3rd exon of NIM1"
                                                                                           LOCATION: 2787..3347
OTHER INFORMATION: /product= "1st exon of NIM1"
                                                                                                                                                                                                                                                   LOCATION: 4586..4866
OTHER INFORMATION: /product= "4th exon of NIM1"
                                                                                                                                                              of NIM1"
                                                                                                                                                                                                                                                                                                                                                 Score 326.8; DB 3;
Pred. No. 1.3e-83;
0; Mismatches 392;
                                                                                                                              NAME/KEY: exon
LOCATION: 3427..4162
OTHER INFORMATION: /product= "2nd exon
           TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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58.6%;
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  single
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Best Local Similarity
                                                                          NAME/KEY: exon
                                       N<sub>O</sub>
                                                                                                                                                                                                                                         NAME/KEY: exon
STRANDEDNESS:
                                    HYPOTHETICAL:
ANTI-SENSE: NC
FEATURE:
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US-08-996-685-1
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3079 CIAAGAAGGAGAAAGACICCAACAACACCGCCGCGGTGAAGCICGAGCITAAGGAGAIIG 3138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 4586..4866
OTHER INFORMATION: /product= "4th exon of NIM1"
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0; Mismatches
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OTHER INFORMATION: /product= "lst exon
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OTHER INFORMATION: /product= "3rd exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: /product= "2nd
APPLICATION NUMBER: US/08/880,179
                                                                        NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC
TELECOMMUNICATION INFORMATION:
                                                                                                                                            TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5655 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                  DNA (genomic)
                                                     ATTORNEY/AGENT INFORMATION:
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HYPOTHETICAL: NO
                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: exon
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; LOCATION:
US-08-880-179-2
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                                                                                              AAGAGGATACATAGGGCATTGGATTCTGATGTTGTAGAATTACTACAAATGTTGCTAAGA 1097
                                                                                                                                                                     GAGGGGCATACTACCTAGATGATGCATATGCTCTCCATTATGCTGTAGCGTATTGCGAT 1157
                                                                                                                                                                                                                                            GCAAAGACTACAGCAGAACTTCTAGATCTTGCACTTGCTGATATTAATCATCAAAATTCA 1217
                       978 TCACGAGCGGAACTTGGTCTACAAGGGCCTGAAAGCAACGGTTTTCCTGATAAACATGTT 1037
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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STREET: 520 White Plains Road, P.O. Box 2005
CITY: Tarrytown
STATE: New York
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Delaney, Terry
Friedrich, Leslie
Weymann, Kristianna
Lawton, Kay
Ellis, Daniel
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Jesse, Taco
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TITLE OF INVENTION: GE
TITLE OF INVENTION: SI
TITLE OF INVENTION: IN
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Pred. No. 1.8e-83;
0; Mismatches 392;
                                  ADDRESSEE: No. 6091004artis Corporation
STREET: 520 White Plains Road, P.O. Box 2005
CITY: Tarrytown
STATE: New York
COUNTRY: USA
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                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/880,179
                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                               CLASSIFICATION CONTROL ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: GGC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8689
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 9919 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 535 AAAAGGAGAAGAATAGTAGT-----
                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15.0%;
58.6%;
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Best Local Similarity 58.6
Matches 714; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                             ZIP: 10591
COMPUTER READABLE FORM:
                       CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 800
       NUMBER OF SEQUENCES:
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US-08-880-179-1
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                                           GATATICTIGACAAAACTGCAGCAGACGATGTAATGATGGTTTTATCTGTTGCAAACATT
                                                                                                    858 TGTGGTAAAGCATGCGAGAGATTGCTTTCAAGCTGCATTGAGATTATTGTCAAGTCTAAT
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Delaney, Terry
Friedrich, Leslie
Weymann, Kristianna
Lawton, Kay
Ellis, Daniel
Uknes, Scott
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Sequence 1, Application US/08880179
Patent No. 6091004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jesse, Taco
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APPLICANT:
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3123 GACGTTGTAGACAAAGTTGTTATAGAGGACACATTGGTTATACTCAAGCTTGCTAATATA 3064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGTGGTAAAGCATGCGAGAGATTGCTTTCAAGCTGCATTGAGATTATTGTCAAGTCTAAT
                                                                                                                            3063 TGTGGTAAAGCTTGTATGAAGCTATTGGATAGATGTAAAGAGATTATTGTCAAGTCTAAT
                                                                                                                                                                                                                                        GAGGGCCATACTACCCTAGATGATGCATATGCTCTCCATTATGCTGTAGCGTATTGCGAT
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                                                                                                                                                                                                GTTGATATCATAACCCTTGATAAAGCCTTGCCTCATGACATTGTAAAACAAATTACTGAT
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Patent No. 5986082
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
APIS, John
TITLE OF INVENTION:
ALTERED FORMS OF THE NIMI GENE CONFERRING
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
ADDRESSEE:
ADDRESSEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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US-08-989-478-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28 AAGCTCGAGCTTAAGGAGATTGCCAAGGATTACGAAGTCGGTTTCGATTCGGTTGTGACT 87
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Pred. No. 4.9e-81;
0; Mismatches 263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-21214/P1/CGC1911
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8687
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product= "Altered form of
/note= "Ankyrin domains of
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                              PRICE APPLICATION DATA:
APPLICATION NUMBER: US 60/033,177
FILING DATE: 13-DEC-1996
PRICE APPLICATION NUMBER: US 60/034,379
FILING DATE: 27-DEC-1996
PRICE APPLICATION NATA:
AP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 60/035,021
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,022
FILING DATE: 10-JAN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.6%;
64.3%;
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TYPE: nucleic acid
STRANDEDNESS: single
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Matches 496; Conservative
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                                                                               CURRENT APPLICATION DATA
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) LOCATION: 1.786

) OTHER INFORMATION: ,

US-08-989-478-15
                                                                                                                     APPLICATION NUMBER: FILING DATE:
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Search completed: October 8, 2002, 01:24:23 Job time: 116.239 secs

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Database : EST:\*

1: em\_estba:\*
2: em\_esthum:\*
3: em\_estin:\*
4: em\_estin:\*
5: em\_estrov:\*
6: em\_estpl:\*
7: em\_estpl:\*
10: qb\_estp:\*
10: qb\_estp:\*
11: qb\_ntc:\*
12: qb\_qss:\*
13: em\_qss\_lnv:\*
14: em\_qss\_lnv:\*
15: em\_qss\_lnv:\*
16: em\_qss\_lnv:\*

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	AW160235 EST290093	RG124935 EST470581	BE435499 EST406577	AW622846 EST306916	BE432768 EST399297	BG464249 EM1 71 D1	BI210424 EST528464	AW160234 FST290092	AV551266 AV551266	BE493178 WHE0570 C	BH525927 BOGTO04TF				AW399343 EST30943	BE918569 OV1 8 E08	AW745943 WS1_38_H0
SUMMARIES	ID	AW160235	BG124935	BE435499	AW622846	BE432768	BG464249	BI210424	AW160234	AV551266	BE493178	BH525927	BM111027	BG598808	BE023215	AW399343	BE918569	AW745943
	DB	6	10	10	6	10	10	10	6	6	10	12	10	10	6	6	10	6
	Query Match Length DB	613	654	736	516	503	614	539	557	573	455	772	700	667	458	450	547	569
ď	Query Match	23.8	21.0	18.4	16.3	16.0	14.6	12.0	11.5	10.8	10.7	9.7	9.1	8.8	8.3	7.9	7.7	7.6
	Score	517.2	457	400.6	354.2	348	316.2	261.2	249	234.2	232	211.2	198.2	191.8	179.6	171.8	167.2	164
	Result No.	П	7	ო	4	വ	9	7	ω	σ	10	11	12	13	14	15	16	17
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	20	161.6	7		10	BF096790	
	21	157	7		10	BM307942	
	22	152.6	7		10	BG414779	
	23	150.2	9		10	BG526766	
J	c 24	146.6	φ		12	B26306	18D8TF
•	2 25	146.4	6.7	730	10	B1968818	B1968818 GM830006B
	56	146	9		0	AI442277	AI442277 sa66a04.y
	27	146	9		δ	AW216501	_
	28	137.4	9		10	BG526883	
	29	131.2	9		10	BG521476	BG521476 10-59 Ste
	30	130.4	9		6	AL372473	AL372473 MtBA51C01
		128.4	LC)		10	BE801977	BE801977 sr23d08.y
J	35	128.4	S.		6	AW310982	AW310982 sg31b02.x
		124.4	LO I		10	BE366197	BE366197 PI1_31_F0
J	34	123.6	D		12	BH483537	BH483537 BOGXP26TF
	32	122.8	ഗ		10	BE366196	
	36	118.6	വ		10	BM324012	
	37	115.8	S		σ	AW687759	_
	38	114.6	S		σ	AW618318	AW618318 EST320304
J		114.4	S		6	A1997958	
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i C	LOCIES		AW160235			613 bm	1 4 4 4
3 2	DEFINITION	•	~	<u>, -</u>	, [ [	orogeniii trichomo	
			pennellii	CDNA cle	one	119 simi	rierr ourversity bycopersicon r to A. thaliana transcription
,			factor inhibitor I kappa	ibitor	ı ka	ppa B homolog,	dnence.
A :	ACCESSION		AW160235		t		
K.	KEYWORDS	EST.	T.	61.6770:T5	0/6/	ν	
SC	SOURCE	LV	Lycopersicon pennellii	on penne	111	-	
	ORGANISM		Lycopersicon	on pennellii	111		
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MANIOUS AND	AW160235 EST290093 L. pennellii trichome, Cornell University Lycopersicon pennellii cDNA clone cLPTI19 similar to A. thaliana transcription factor inhibitor I kappa B homolog, mRNA sequence. AW160235 AW160235.1 GI:6279769 EST. Lycopersicon pennellii.
ORGANISM ORGANISM AUTHORS	Lycopersicon pennellii Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Bukaryota; Viridiplantae; Streptophyta; Core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum; Lycopersicon. I (bases I to 613) Alcala,J., Vrebalov,J., White,R., Matern,A.L., Lakey,J., Holt,I.E., Liang,F., Hansen,T.S., Upton,J., Ronning,C.M., Craven,M.B., Fujii C.Y., Bowman,C.L., Nlerman,W., Fraser,C.M., Venter,J.C., Martin G.B., Tanksley,S.D. and Glovannoni,J.
TITLE JOURNAL COMMENT	Generation of ESTs from wild tomato (Lycopersicon pennellii) trichomes Unpublished (1999) Contact: CHGI Clemson University Genomics Institute Clemson University 100 Jordan Hall, Clemson, SC 29634, USA Email: http://www.genome.clemson.edu/orders/index.html 3 prime sequence.
FEATURES	Location/Qualifiers  1. 613  /Organism="Lycopersicon pennellii" /db_xref="taxon:28526" /db_cref="taxon:28526" /clone="clpTl19" /clone_lib="trichome" /dev_stage="mixed stages" /lab_host="SOLR" /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Leaves of various stages were shaken in liquid

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Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                        Local
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                                                                                                                                                                                                                                                                   BASE COUNT
ORIGIN
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Matches
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        JOURNAL
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                                                                                   FEATURES
                    COMMENT
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nitrogen, shearing off trichomes. This procedure yielded a mixture of cells highly enriched for trichomes, with minor contamination by other types of leaf cells."
                                                                                                              2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     654 bp mRNA linear EST 31-JAN-2001 tomato shoot/meristem Lycopersicon esculentum cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lycopersicon esculentum
Sukaryota, Vitidiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 654)
van der Hoeven, R., Bezzerides, J., Sun, H., Cho, J., Utterback, T.,
Hansen, C., Ronning, C. and Tanksley, S.
Generation of ESTs from tomato shoot/meristem tissue
                                                                                                                                                                                        1729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACTGAAGAAGCAAAGGTACATGGAACTTCAAGAAATTCTGACTAAAGCATTCACTGAGGA 1909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1970 AGTAGATAAGCCCAATAAGCTCCCTTTTAGGAAATAGGTAATTGTATTAGGATATATAGA 2029
                                                                                                                                                                                                                                           CCTTTTTCCAATGGAAGCTAAAGTTGCAATGGACATTGCTCAAGTTGATGGCACTTCTGA 1609
                                                                                                                                                                                                                                                                                              GTTCCCACTGGCTAGCATCGGCAAAAAGATGGCTAATGCACAGAGGACAACAGTAGATTT 1669
                                                                                                                                                                                                                                                                                                                                                                                                    AACTGTAGAACTTGGAAAACGCTTCTTTCCACGTTGTTCAGAAGTTCTAAATAAGATCAT 1789
                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGATGCTGATGACTTGTCTGAGATAGCTTACATGGGGAATGATACGGCAGAAGAGCGTCA 1849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAAAGAAGAATATGATAAGACTAACAACATCTCCTCATCTTGTTCCTCTACATCTAAGGG 1969
                                                                                                                                       1430 GGAGCAAGCAGAAAGAAGAGCCCTCTGCTAGGAGAAGCTTCTGTATCTCTTGCTATGGC 1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  253 GGATGCTGATGACTTATCTGAGATAGCTTACATGGGGAATGATACAGTAGAAGAGCGTCA 194
                                                                                                                                                                                                                                                          193 ACTGAAGAAGCAAAGGTACATGGAACTTCAAGAATTTTGTCTAAAGCATTCACGGAGGA 134
                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          133 TAAAGAAGAATTGCTAAGACT---AACATGTCCTCATCTTGTTCCTCTACATGTCTAAGGG
                                                                                                                                                                                                                                                                                                            GAACGAGGCTCCTTTCAAGATAAAAGAGGAGCACTTGAATCGGCTTAGAGCACTCTCTAG
                                                                                                                                                                                                                                                                                                                                                                                                                 4;
                                                                                   Length 613;
                                                                                                              Indels
                                                                                                              38;
                                                                                   Score 517.2; DB 9;
Pred. No. 9.1e-104;
0; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST470581 tomato shoot/meristem Lyroforst 5' sequence, mRNA sequence BG124935
BG124935.1 GI:12625123
                                                                                     23.8%;
                                                                                                     Best Local Similarity 93.1
Matches 564; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lycopersicon.
1 (bases 1 to
                                                                                                    Similarity
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                                                                                       Query Match
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KEYWORDS
SOURCE
ORGANISM
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DEFINITION
                                               COUNT
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BG124935
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ORIGIN
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/note="Vector: pBluescript SK(-); Site_1: EcoR1; Site_2: Xhol: Small expanding leaves from the growing tip were taken from greenhouse plants (4-6wks old TA496). Tissue was immediately frozen in liquid nitrogen."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          1497 GATITGCGTAIGAAGCIGITATACCTIGAAAATAGAGTIGGCCIGGCTAAACTCCTTTT 1556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1557 CCAATGGAAGCTAAAGTTGCAATGGACATTGCTCAAGTTGATGGCACTTCTGAGTTCCCA 1616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           576
                                                                                                                 /organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="TOF7K1"
/clone="ID="tomato shoot/meristem"
/tissue_type="aboot/meristem"
/dev_stage="developing shoots from 4-6wks old plants"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                421
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                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1797 GATGACTTGTCTGAGATAGCTTACATGGGGAATGATACGGCAGAAGAGCGTCAACTGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------ACACAGGACTCTTTTTTTTTTTGAT------GCATACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 GATTTGCGTATGAAGCTGTTATACCTTGAAATAGAGTTGGTCTGGCTAAACTCCTTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1617 CTGGCTAGCATCGGCAAAAAAAGATGCCTAATGCACAGAGGACAACAGTAGATTTGAACGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   302 GATGACTTGTCTGAGATAGCTTACATGGGGAACGATACAGTAGAAGAGCGTCAACTGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1857 AAGCAAAGGTACATGGAACTTCAAGAAATTCTGACTAAAGCATTCACTGAGGATAAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1917 GAATATGATAAGACTAACAACATCTCCTCATCTTGTTCCTCTACATCTAAGGGAGTAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25;
Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                    Length 654;
                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                    Score 457; DB 10;
Pred. No. 1.8e-90;
0; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AACAGCTGTACCATAAACTTGTATTGT 2123
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                                                                                                                                                                                                                                                                                                                                                                                        21.0%;
88.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                            552; Conservative
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846

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l (bases I to 516)
van der Hoeven, R.S., Bezzeredes, J.L., Matern, A.L., Holt, I.E., Liang
van der Hoeven, R.S., Bezzeredes, J.L., Ronning, C.M., Nierman, W.,
F., Hansen, T., Craven, M.B., Bowman, C.L., Ronning, C.M., Nierman, W.,
Generation of ESTs from tomato flower tissue, 3-8 mm buds
Contact: CUGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="crobs42"
/clone_lib="tomato flower buds 3-8 mm, Cornell University"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lycopersicon esculentum
Eukaryota, Viridiplantee, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnollophyta; eudicotyledons; core eudicots;
Asteridae, euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="flower"
/dev_stage="3-8mm buds"
/dev_stage="3-8mm buds"
/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
Xho1; supplier: Tanksley; Flower buds and flowers were
taken from greenhouse plants (4-8 wks old, 7A496). They
were immediately frozen in liquid nitrogen and then
size-separated while remaining frozen."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1609 AGTICCCACTGGCTAGCATCGGCAAAAAGATGGCTAATGCACAGAGGACAACAGTAGATT 1668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1669 TGAACGAGGCTCCTTTCAAGATAAAAGAGGAGCACTTGAATCGGCTTAGAGCACTCTCTA 1728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           516 bp mRNA linear EST 18-MA buds 3-8 mm, Cornell University CDNA clone CTOB5H2 5', mRNA sequence.
        787 GACACCTACTGGATATTCTTGACAAAACTGCAGCAGACGATGTAATGGTTTTTATCTG
                                                                                                                                                                                                                                          GTGTTTGTGTGGACAATGACTGCTCTCATGTGGCCTTGTAGGCCAGCTGTGGCATTCCTGG
                                                                                                                                         727 TTGAGGTTTTGTACACATCATTTACCTTTCAGATCTCTGAATTGGTTGACAAGTTTCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clemson University Genomics Institute
clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 516;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                   Score 354.2; DB 9;
Pred. No. 8.6e-68;
0; Mismatches 28;
                                                                                                                                                                                                                                                                                                   TTGCAAACATTTGTGGTAAAGCATGCGAGAGATTGCTTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST306916 tomato flower
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AW622846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AW622846.1 GI:7335873
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92.5%;
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395; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tomato.
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Best Local S
Matches 395,
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AW622846/c
LOCUS
DEFINITION
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JOURNAL
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: pBluescriptSKmCUadapt; Site_1: EcoRl; Site_2: XhoI; Fruit were harvested at the breaker stage (first sign of lycopene accumulation on the blossom end of the fruit). Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp."
                    BE435499 736 bp mRNA linear EST 18-MAY-2001 EST406577 tomato breaker fruit, TIGR Lycopersicon esculentum cDNA clone cLEG27M10, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3;
                                                                                                                                                                                                                                                1 (bases 1 to 736)
Alcala, J., Vrebalov, J., White, R., van der Hoeven, R.S., Holt, I.E., Liang, F., Hansen, T.S., Craven, M.B., Bowman, C.L., Ronning, C.M., Nierman, W., Fraser, C.M., Martin, G.B., Giovannoni, J.J. and Tanksley
                                                                                                                                                   Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  247 ATAGTAGGACTGCGTTTTCTGATTCGAATGACATCAGCGGAAGCAGTAGTATATGCTGCA 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCGCCGCCGCCATGAATTTTTCTCGCCGGAGACTTCGCCGGCGGAGATCACTTCAC 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      367 IGAAACGCCTATCGGAAACACTGGAATCTATCTTCGATGCGTCTTTGCCGGAGTTTGACT 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        607 IAATGAGTGTATTGGCTTATTTGTATAGTGGTAAAGTTAGGCCCTTCACCTAAAGATGTGT 666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              487 GCATTTTGTCGGCGAGGAGTCCGTTCTTTAAGAATTTGTTCTGCGGTAAAAGGAGAAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           547 ATAGTAGTAAGGTGGAATTGAAGGAGGTGATGAAAGAGCATGAGGTGAGCTATGATGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Generation of ESTs from tomato fruit tissue, breaker stage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACTICGCCGACGCTAAGCTTGTGGTTTCCGGCCCGTGTAAGGAAATTCCGGTGCACCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 736;
                                                                                                                                                                                                                                                                                                                                                                                                        Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 400.6; DB 10; Length
Pred. No. 4.9e-78;
0: Mismatches 94; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="cligg27M10"
/clone_lib="tomato breaker fruit, TIGR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Lycopersicon esculentum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="Pericarp"
/dev_stage="breaker"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cultivar="TA496"
/db_xref="taxon:4081"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                           BE435499.1 GI:9433342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tch 18.4%; sl Similarity 80.7%; 517; Conservative
                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2000)
Contact: CUGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     prime sequence.
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                                                                                                                                   tomato
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Gaps

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EST 18-MAY-2001

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Sorghum bicolor

Sorghum bicolor

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida: Poales; Poaceae; PACC
cladd; Panicoldeae; Andropogoneae; Sorghum.

E 1 (bases 1 to 614)

S Reid,S.P., Cordonnier-Pratt,M.-M., Gingle,A. and Pratt,L.H.
An EST database from Sorghum: developing embryos

L Onpublished (2000)

Tontact: Cordonnier-Pratt MM
Department of Botany
The University of Georgia

Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              butot249 614 bp mRNA linear EST 20-MAR-2001
EM1,71_D12.b1_A002 Embryo 1 (EM1) Sorghum bicolor cDNA, mRNA
sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to exclude PolyA, vector and regions threshold for highest quality sequence
                                                                                                                                                                                                                                                                                                                                                                                               TCTTCGATGCGTCTTTGCCGGAGTTTGACTACTTCGCCGACGCTAAGCTTGTGGTTTCCG 456
                                                                                                                                                                                                         126 GC---GGTAAGGAAATTCCGGTGCATCGGTGCATTTTGTCGGCGAGGAGTCCTTTTTTA 182
                                                                                                                                                                                                                                                          TGAAAGAGCATGAGGTGAGCTATGATGCTGTAATGAGTGTATTGGCTTATTTGTATAGTG 636
                                                                                                                                                                                                                                                                                                                                               TGGCTTGTAGGCCAGCTGTGGCATTCCTGGTTGAGGTTTTGTACACATCATTTACCTTTC 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    816
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                                                                                                                                      GCCCGTGTAAGGAAATTCCGGTGCACCGGTGCATTTTGTCGGCGAGGAGTCCGTTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGATCTCTGAATTGGTTGACAAGTTTCAGAGACACCTACTGGATATTCTTGACAAAACTG
                6
                Indels
              16;
              Mismatches
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 Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: mmpratt@uga.edu
Sequences have been trimmed
below Phred quality 16. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq primer: JEN REV
High quality sequence stop:
                0;
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83.28;
 Similarity 83.2 (2); Conservative
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BG464249.1
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                  422;
   Local
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST 18-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lycopersicon.
1 (bases 1 to 503)
Alcala,J., Vrebalov,J., White,R., van der Hoeven,R.S., Holt,I.E.,
Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Ronning,C.M.,
Nierman,W., Fraser,C.M., Martin,G.B., Glovannoni,J.J. and Tanksley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lycopersicon esculentum
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Asteridae, euasterids I; Solanales, Solanaceae, Solanum,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  503 bp mRNA linear EST 18-MAY-200
85399297 tomato breaker fruit, TIGR Lycopersicon esculentum CDNA
clone cLEG10A24, mRNA sequence.
                                      1788
                                                                                                         1789 TGGATGCTGATGACTTGTCTGAGATAGCTTACATGGGGAATGATACGGCAGAAGAGCGTC 1848
                                                                                                                                                                            1849 AACTGAAGAAGCAAAGGTACATGGAACTTCAAGAAATTCTGACTAAAGCATTCACTGAGG 1908
                                                                                                                                                                                                                                               ATAAAGAAGAATATGATAAGACTAACAACATCTCCTCATCTTGTTCCTCTACATCTAAGG 1968
                                                                                                                                                                                                                                                                                                                  1969 GAGTAGATAAGCCCAATAAGCTCCCTTTTAGGAAATAGGTAATTGTATTAGGATATAGA 2028
   337
                                                                                                                                                                                                                                                                                                                                    GAACTGTAGAACTTGGAAAACGCTTCTTTCCACGTTGTTCAGAAGTTCTAAATAAGATCA
                                                        276 AACTGAAGAAGCAAAGGTACATGGAACTTCAAGAAATTTTGTCTAAAGCATTCACGGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Generation of ESTs from tomato fruit tissue, breaker stage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Lycopersicon esculentum"
/oultivar="TA496"
/db_xref="taxon:4081"
/clone="ciegloA24"
/clone=lib="tomato breaker fruit, TIGR"
/lasue_type="Pericarp"
/lab_host="SOLR"
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1. .503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2000)
Contact: CUGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prime sequence.
                                                                                                                                                                                                                                                                                                                                                                                     GGAAGAA 2035
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                                                                                                                                                                                                                                                                                                                                                                                                                      GGAAGAA 94
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JOURNAL
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BE432768
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//note—Vector: Bluescript SK(-); Site 1: EcoRI; Site_2:
XhoI; Suspension cultures of L.esculentum E6203 were grown
in Murashige and Skoog based medium, supplemented with 15%
coconut milk (filter sterilized and added after
autoclaving), 2% saccharose, and Img/ml 2,4D (pH5.8).
Fresh medium was added every 7 days, and cultures were
strown at 25 C, with 12hrs of light and continuous
shaking."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST 18-MAY-2001
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1 (bases 1 to 539)
van der Hoeven, R., Sun, H., Bezzerides, J., Cho, J., Utterback, R., Ronning, C. and Tanksley, S.
Generation of ESTs from Tomato Suspension Cultures
Unpublished (2001)
Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1784 GATCATGGATGCTGATGACTTGTCTGAGATAGCTTACATGGGGAATGATACGGCAGAAGA 1843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCGTCAACTGAAGAAGCAAAGGTACATGGAACTTCAAGAAATTCTGACTAAAGCATTCAC 1903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1904 IGAGGATAAAGAAGAATATGATAAGACTAACAACATCTCCTCTTGTTCCTCTACATC 1963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAAGGGAGTAGATAAGCCCCAATAAGCTCCCTTTTAGGAAATAGGTAATTGTATTAGGATA 2023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1724 CICTAGAACTGTAGAACTTGGAAAACGCTTCTTTCCACGTTGTTCAGAAGTTCTAAATAA 1783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2084 TCAACATACATACAACAGCTGTACCATAAACTTGTATTGTTGCACTTACAACTTTGAAGA 2143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  297 TATGAGGAAGAAACACAGGACTCTCTTTCTT----TTTCATCATTTGATGCATACAAAAC 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  353 ACATGTACCATAAACTTGTATTGTGAAAAAAGATAAAATTTCATTATTAGTTGAGAAGG 412
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8
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                                                                                                                                                                                                                           esculentum"
                                                                                                                                                                                                                                                                                                                 /tissue_type="suspension cultures"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12.0%; Score 261.2; DB 78.6%; Pred. No. 2.9e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                     /organism="Lycopersicon e/cultivar="TA496, E6203"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:4081"
                                                                                                                                                                                                                                                                                              /clone_lib="cTOS"
                                                                                                                                                                                                                                                                              /clone="cTOS23C4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 352; Conservative
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                          AUTHORS
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       REFERENCE
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LOCUS
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             /clone_lib="Embryo 1 (EM1)"
/note="Organ: Embryos germinated for 24 hr; Vector:
pBluescript II from Lambda Zap II; Site_1: XhoI; Site_2:
ECORI; The library was made from poly-A RNA in the cloning vector lambda Zap II. Clones to be sequenced were
                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BI210424 539 bp mRNA linear EST 11-JUL-2001 EST528464 CTOS Lycopersicon esculentum CDNA clone CTOS23C4 5' end,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                         996 CTACAAGGCCCTGAAAGCAACGGTTTTCCTGATAAACATGTTAAGAGGATACATAGGGCA 1055
                                                                                                                                                                                                                                                                                                                                                                                              1056 ITGGATTCTGATGATGTTGAATTACTACAAATGTTGCTAAGAGAGGGGCATACTACCTA 1115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1116 GATGATGCATATGCTCTCCATTATGCTGTAGCGTATTGCGATGCAAAGACTACAGCAGAA 1175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1236 CATGTTGCAGCCATGAGGAAAGAGCCTAAAATTGTAGTGTCCCTTTTAACCAAAGGAGCT 1295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1296 AGACCTICTGATCTGACATCCGATGGAAGAAAGCACTTCAAATCGCCAAGAGGCTCACT 1355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1356 AGGCTIGIGGATTICAGTAAGTCTCCGGAGGAAGGAAAATCTGCTTCGAATGATCGGTTA 1415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1416 TGCATTGAGATTCTGGAGCAGAAGAAGAAGACCCTCTGCTAGGAGAAGCTTCTGTA 1475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1476 TCTCTTGCTATGGCAGGCGATGATTTGCGTATGAAGCTGTTATACCTTGAAAATAGAGTT 1535
                                                                                                                                                                                                                                                                                                                                               247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        936 GATAAAGCCTTGCCTCATGACATTGTAAAACAAATTACTGATTCACGAGCGGAACTTGGT
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0
                                                                                                                                                                                    Length 614;
                                                                                                                                                                              Score 316.2; DB 10; Length
Pred. No. 2.1e-59;
0; Mismatches 178; Indels
                                                                                                          by mass excision."
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                                                                                                                                                                                Query Match
Best Local Similarity 70.4%;
Matches 423; Conservative
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BI210424
LOCUS
DEFINITION
                                                                                                                           BASE COUNT
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519 GIGTITGIGIGGACAAIGAGIGCIIGCAIGIAGCIIGIA 557

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Arabidopsis thaliana
Arabidopsis thaliana
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases I to 573)
Asamizu.E., Nakamura,Y., Sato,S. and Tabata,S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
DNA Res. 7, 175-180 (2000)
                                                                                        AV551266 Arabidopsis thaliana roots Columbia Arabidopsis thaliana cDNA clone RZ123e05R 5', mRNA sequence.
AV551266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The First Laboratory for plant Gene Research
Kazusa DRA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizuékazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="roots"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1207 ATCAAAATTCAAGGGGATACACGGTGCTGCATGTTGCAGCCATGAGGAAAGAGCCTAAAA 1266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     967 AAATTACTGATTCACGAGCGGAACTTGGTCTACAAGGGCCTGAAAGCAAGGTTTTCCTG 1026
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGTATTGCGATGCAAAGACTACAGCAGAACTTCTAGATCTTGCACTTGCTGATATTAATC 1206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 234.2; DB 9;
Pred. No. 2.6e-41;
0; Mismatches 198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .573
/organism="Arabidopsis thaliana"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    strain="Columbia"
/db_xref="taxon:3702"
/clone="RZ123e05R"
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                                                                                                                                                                              AV551266.1 GI:8722679
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ilarity 64.1%;
Conservative C
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Matches 375;
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MEDLINE
COMMENT
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AUTHORS
TITLE
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                                                                                                                                                                                VERSION
KEYWORDS
SOURCE
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                                                       RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note-"Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Leaves of various stages were shaken in liquid nitrogen, shearing off trichomes. This procedure yielded a mixture of cells highly enriched for trichomes, with minor contamination by other types of leaf cells."
                                                                                                                                                                                  Holt, I.E.,
B., Fujii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3;
                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                               Alcala,J., Lakey,J., White,R., Matern,A.L., Lakey,J., Holt,I.E. Alcala,J., Vrebalov,J., White,R., Matern,A.L., Lakey,J., Holt,I.E. Liang,F., Hansen,T.S., Upton,J., Ronning,C.M., Craven,M.B., Fujli,C.Y., Ewman,C.L., Nierman,W., Fraser,C.M., Venter,J.C., Martin,G.B., Tanksley,S.D. and Giovannoni,J. Generation of ESTs from wild tomato (Lycopersicon pennellii)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cornell University"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              129 ATAGTAGAACTGCTTTTTCGGATTCCAATGATATTAGTGGAAGCAGTAGTATATGCTGCA 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       247 ATAGTAGGACTGCGTTTTCTGATTCGAATGACATCAGCGGAAGCAGTAGTATATGCTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCGGCGGCGGCATGACTGAATTTTTCTCGCCGGAGACTTCGCCGGCGGAGATCACTTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      367 TGAAACGCCTATCGGAAACACTGGAATCTATCTTCGATGCGTCTTTGCCGGAGTTTGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          288 TCTTCGCTGATGCGAACTTCTGGCTCCAGGC---GGTAAGGAAATTCCGGTGCACGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCATTTTGTCGGCGAGGAGTCCGTTCTTTAAGAATTTGTTCTGCGGTAAAAAGGAGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCATTTTGTCGGCGAGGAGTCCTTTTTTAAGAATGTATTCTGTGGGAAA-----GATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            399 GCAACACGAAGCTGGAACTCAAAGAGCTGATGAAAGAGTATGAGGTGAGTTTTGATGCGG
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                                                                                                                                                                                                                                                                                                                              Confact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Lycopersicon pennellii"
/db_xref="taxon:28526"
/clone="clpriig"
/clone_lib="L. pennellii trichome,
/tissue_type="trichome"
/dev_stage="mixed stages"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.5%; Score 249; DB 9; Le
ilarity 77.1%; Pred. No. 1.4e-44;
Conservative 0; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GIGITIGIGIGACAATGACTGCTCTCATGTGGCTTGTA 705
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab_host-"SOLR"
    GI:6279768
                                             Lycopersicon pennellii
                                                                                                                                                                                                                                                                                         trichomes
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                   prime sequence.
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                                                                  Lycopersicon
                                                                                                                                                  Lycopersicon
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nes 354; Conserv
AW160234.1
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GSS 13-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brassica oleracea
Brataryora, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                             953 TGACATTGTAAAACAAATTACTGATTCACGAGCGGAACTTGGTCTACAAGGGCCTGAAAG 1012
                                                                                                                                                                                                                                                                                                                                                                    1073 TGAATTACTACAAATGTTGCTAAGAGGGGGCATACTACCTAGATGATGATGCTGT 1132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1133 CCATTATGCTGTAGCGTATTGCGATGCAAAGACTACAGGCAGAACTTCTAGATCTTGCACT 1192
                                                                                                                                                                                                                                               .013 CAACGGTTTTCCTGATAAACATGTTAAGAGGATACATAGGGCCATTGGATTCTGATGATGT 1072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGCTGATATTAATCATCAAAATTCAAGGGGATACACGGTGCTGCATGTTGCAGCCATGAG 1252
                                                                                                                                                                                                                                                                                 248 GGAGCTTGTCAGGATGCTGCTCACAGAGGGCAGACTAACCTTGATGATGCATTTGCATT 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         893 CATTGAGATTATTGTCAAGTCTAATGTTGATATCATAACCCTTGATAAAGCCTTGCCTCA 952
                                                                   68 CCTGGAGATGGTAGTCCGGTCAAATCTTGACATGATTACTCTTGAGAAAGCATTGCCTGA 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        934 TTGATAAAGCCTTGCCTCATGACATTGTAAAACAAATTACTGATTCACGAGCGGAACTTG 993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12; Gaps
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BOGTO04TF BOGT Brassica oleracea genomic clone BOGTO04, DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       308 GCACTATGCTGTAGAACACTGTGACTCAAAAATTACAACAGAACTTCTGGACATCGCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 12; Length 772;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TF
Class: sheared ends.
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/db_xref="taxon:3712"
/clone="BOGT"
/clone="Ub=BOGT"
/note="Vector: PHOS1; Site_1: BstX1; 2-3 kb
genomic DNA inserted into PHOS1 using BstXI
187 c 176 g 210 t
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Town.C.D., Van Aken,S., Utterback,T. and Fraser,C.M. Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001)
Other_GSSS: BOGTO04TR
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61.0%; Pred. No. 3.1e-36;
Live 0; Mismatches 223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
1. .772
/organism="Brassica oleracea"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1253 GAAAGAGCCTAAAATTGTAGTGTCCCTT 1280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      428 GAGAGATCCTAAAATTGTTGTCTTCCTT 455
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Matches 367; Conservative
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Fax: 301-838-0208
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Eukaryota; Viridiplantae: Streptophyta; Embryophyta; Tracheophyta; Spermatophyta: Magnoliophyta; Liliopsida: Poales; Poaceae; Pooideae; Triticeae; Triticum. Nation., Na
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2001)
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="Vegetative shoot apex"
/dev_stage="Three weeks-old plants"
/dev_stage="Three weeks-old plants"
/note="E. coli XLOLR"
/note="Vector: Lambda pBK-CMV (Lambda Zap Express),
excised phagemid; Site_1: EcoRI; Site_2: XhoI; The tissue,
total RNA, and poly(A) RNA were prepared, a cDNA library
was made, and the cDNA clones were in vivo excised at the
University of California, Davis (V. Echenique, B. Stamova
J. Dubcovsky). Plasmid DNA preparations and DNA
sequencing were performed in the OD Anderson lab (all
                                                                                                                                                                                                                                                                                                                                                                                                                                                    BE493178 455 bp mRNA linear EST 16-APR-2001 WHE0570_C11_F222E Triticum monococcum vegetative apex cDNA library Triticum monococcum cDNA clone WHE0570_C11_F22, mRNA sequence.
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1327 AAGCACTICAAATCGCCAAGAGGCICACTAGGCITGIGGAITITCAGIAAGICICCGGAGG 1386
                                                                                                                    AAGGAAAATCTGCTTCGAATGATCGCTTATGCATTGAGATTCTGGAGCAAGGAAAGAA 1446
                                                       409 CCGCACTCATGATCGCAAAACAAGCCACTATGGCGGTTGAATGTAATAATAATATCCCGGAGC 468
                                                                                                                                                      833 GATGGTTTTATCTGTTGCAAACATTTGTGGTAAAGCATGCGAGAGATTGCTTTCAAGCTG 892
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/cultivar="DV92"
/db_xref="taxon:4568"
/clone="WHF0570_cll_F22"
/clone="Iriticum monococcum vegetative apex cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: Stratagene T3 primer.
Location/Qualifiers
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                                                                                                                                                                                                                                1447 GAGACCCTCTGCTAGGAGAGCTTCTGTATCTCTTGCTATGGCAG 1491
                                                                                                                                                                                                                                                                     Pred. No. 8.1e-41;
0; Mismatches 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.7%; Score 232; DB 10; 69.9%; Pred. No. 8.1e-41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BE493178.1 GI:9659771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Triticum monococcum.
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1 (bases 1 to 700)
wan der Hoeven, N., Sun, H., Karamycheva, S. A., Tsai, J., Van Aken, S., Utterback, T., Chiemingo, A., Bougri, O., Buell, C.R., Ronning, C., Tanksley, S. and Baker, B.
                                                                                                     CATTGGATTCTGATGATGTTGAATTACTACAAATGTTGCTAAGAGAGGGGCATACTACCC 1113
                                                                                                                                                                1114 TAGATGATGCATATGCTCTCCATTATGCTGTAGCGTATTGCGATGCAAAGACTACAGCAG 1173
                                                                                                                                                                                                                        AACTICIAGAICTIGCACTIGCTGATATIAAICAICAAAAITCAAGGGGATACACGGTGC 1233
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                                                                                                                                                                                                                                                                                                                                                                                                       CTAGGCTTGTGGATTTCAGTAAGTCTCCGGAGGAAGGAAAATCTGCTTCGAATGATCGGT 1413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                424 CGAATGCGTCGGAGACGACGTTTGACGGTAGAACGCTCTGGTGATTGCGAAAAGGCTCA 365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TATGCATTGAGATTCTGGAGCAAGCAGAAGAAGAAGACCCTCTGCTAGGAGAAGCTTCTG
                                                                         712 GTCTCGAGCCGCCCGA------GCCGGATAAACATGTCATGAACATATACAAGG
                                                                                                                      CCCTTGACTCCGACGATGTTGACCTTGTCAAGATGCTTTTTGACAGAAGACACACGAGTC
                                                                                                                                                                                GTCTACAAGGGCCTGAAAGCAACGGTTTTCCTGATAAACATGTTAAGAGGATACATAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Generation of ESTs from potato roots
Uppublished (2001)
Contact: Research Genetics, Libraries Division
Tel: 1-800-711-6195
Email: cdnefresgen.com
For clone info: please contact Research Genetics, I
Division tel 1-800-711-6195, email cdnefresgen.com
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Solanum tuberosum
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/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: KhoI; supplier: Corneil University, Tanksley lab; sequencing; The Institute for Genomic Research. Roots were isolated from in vitro grown stem cuttings on CM medium. Roots were isolated two weeks after placing the stem cuttings from in vitro grown plants on medium."
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1 (bases 1 to 667)

wan der Hoeven, W., Bezzeridaes, J., Sun, H., Cho, J., Chiemingo, A., Bougri, O., Buell, C.R., Ronning, C., Tanksley, S. and Baker, B. Generations of ESTs from sprouting potato eyes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITCCTGATAAACATGTTAAGAGGATACATAGGGCATTGGATTCTGATGATGTTGAATTA 1079
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        581 ATGCGTCACAACCCAATGACCGGAGATGCATTATTTTCTTCCCCCATGTTGGCCGATGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 700;
                  /clone="cPRO10C3"
/clone_lib="potato roots"
/tissue_type="roots"
/dev_stage="roots"
/dev_stage="in vitro grown stem cuttings"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       213; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                              Score 198.2; DB 1 Pred. No. 2.3e-33;
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/db_xref="taxon:4113"
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'Supernod' plants generously donated by Dr. Gary Stacey.
The seedlings were innoculated with Bradyrhizobium
japonicus, strain USDAILO priot to harvest. Stratagene's
CDNA synthesis Kit (catalog number 200401) was used to
synthesize the CDNA. First-strand synthesis was performed
with Smethyl dCTP, hence the ligated CDNA was
hemimethylated. A modification of Stratagene's
first-strand synthesis primer was used. An 'anchor'
nucleotide (VaA.C, or G) was added to the 3' end of the
primer [GAGAGAGAGAGAGAGAACATGTCTCGAG[T]]89] to anchor
the primer [GAGAGAGAGAGAGAGAACATGTTCTCGAG[T]]89] to anchor
the primer at the 5' end of the poly(A) tract. After
second strand synthesis, the CDNA ends were filled in with
cloned Pfu DNA polymerase, ligated to EcoRI adapters and
subsequently phosphorylated. The XhoI site within the
first-strand synthesis primer was then restricted by
digestion with XhoI; all XhoI sites in the CDNA would be
protected by their hemimethylated status. The CDNA
constructs were size-fractionated with a 500bp cutoff,
using GibcoBRL Life Technologies' CDNA Size Fractionation
Stratagene's palluescript II XR Predigested vector
(pBluescript II SK(+) that has been digested with EcoRI
and XhoI, and phosporylated by Stratagene). Both the
white and blue colonies appear to contain recombinant
plasmids with CDNA inserts, based on size (n=25). This
library was constructed by Dr. Paul Keim and Dr. Virginia
sm70a04.yl Gm-c1028 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1028-9223 5' similar to TR:081848 081848 HYPOTHETICAL 68.2 KD
PROTEIN. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This clone is available through: ResGen, Invitrogen Corp. 2130 south Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact via email: ccueresgen.com
                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 458)
Shoemaker, R. Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M. Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
Unpublic Soybean EST project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: pBluescript II XR; Site_1: EcoRI; Site_2: XhoI; The mRNA was isolated from roots of Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1028-9223"
/clone_lib="Gm-c1028"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
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                                       DEFINITION
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ORIGIN
                                                                                                                                                                                                                                                                                                                                       REFERENCE
AUTHORS
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JOURNAL
                                                                                                                ACCESSION
                                                                                                                                     VERSION
KEYWORDS
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                                                                                                                                                                                         SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; Various sizes of sprouting eyes (2mm to 15mm) were taken from tubers. The tubers were incubated at 26C in the dark for 2-3 weeks prior to sprouting. The eyes were frozen in liquid nitrogen immediately upon removal from tubers."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST 03-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1026 GATAAACATGTTAAGAGGATACATAGGGCATTGGATTCTGATGATGTTGAATTACTACAA 1085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1086 ATGTTGCTAAGAGGGGCATACTACCCTAGATGATGCATATGCTCTCCATTATGCTGTA 1145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1203 AATCATCAAAAATTCAAGGGGATACACGGTGCTGCATGTTGCAGCCATGAGGAAAGAGCCT 1262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1263 AAAATTGTAGTGCCCTTTTAACCAAAGGAGCTAGACCTTCTGATCTGACATCCGATGGA 1322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1503 CGTATGAAGCTGTTATACCTTGAAAATAGAGTTGGCCTGGCTAAACTCCTTTTTCCAATG 1562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1146 GCGTATTGCGATGCAAAGACTACAGCAGAACTTCTAGATCT---TGCACTTGCTGATATT 1202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1323 AGAAAAGCACTTCAAATCGCCAAGAGGCTCACTAGGCTTGTGGATTTCAGTAAGTCTCCG 1382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1443 AGAAGACCCTCTGCTAGGAGAAGCTTCTGTATCTCTTGCTATGGCAGGCGATGATTTG 1502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242 TCAATAATAATGGGACTACTTGCAAAAGGAGCATCGGTCTTGGATACTACACGCGACGGA 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        422 ATTAGGAATCCTATGATTGGGAGCATGTCTTCTTCATCATTGGTGTTGGTGATTA 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 GAAAAGAGAATTAGGAGATTCTGAAGGCTCTGGAGTCTGATGAACTTGAACTGCTAACA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTCATGAGGTTGCTTTTATTTGAAAATAGAGTGGCATTGGCACGGATGTTATTTCCTCAG 541
                                                 Contact: Cathy Rouning
The Institute for Genomic Research
For clone info: please contact Research Genetics, Libraries
Division tell 1-800-711-6195, email cdna@resgen.com
Seq primer: M13F-R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 GCCTATTGCAACTCCAAGGTTGTGAACGAGGTACTTGAGCTGGGTTTAGGCGCTGATGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 667;
                                                                                                                                                                                                                                                                                                                                                              from tubers"
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                                                                                                                                                                                                                                                                                                                                                         /tissue_type="sprouting eyes from tub
/dev_stage="12-14 weeks post harvest"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAAGCCATGCTAGCTATGGAAATAGCACATGCTGATTCAACCGCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 191.8; DB 10;
Pred. No. 6e-32;
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                                                                                                                                                                                                                           /organism="Solanum tuberosum"/cultivar="Kennebec"
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                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                                                                          /clone="cSTS22E2"
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Similarity 59.1%;
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AW399343 450 bp mRNA linear EST 18-MAY-2001 EST309843 L. pennellii trichome, Cornell University Lycopersicon pennellii cDNA clone cLPT7013 5', mRNA sequence.
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Alcala,J., Vrebalov,J., White,R., Matern,A.L., Lakey,J., Holt,I.E., Liang,F., Hansen,T.S., Upton,J., Ronning,C.M., Craven,M.B., Fujii,C.Y., Bowman,C.L., Nierman,W., Fraser,C.M., Venter,J.C., Martin,G.B., Tanksley,S.D. and Glovannoni,J.
Generation of ESTs from wild tomato (Lycopersicon pennellii)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lycopersicon pennellii
Sukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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/tissue_type="trichome"
                                                                                1036 TTAAGAGGATACATAGGGCATTGGATTCTGATGATGTTGAATTACTACAAATGTTGCTAA 1095
                                                                                                                                                                     1096 GAGAGGGCATACTACCTAGATGATGCATATGCTCTCCATTATGCTGTAGGGTATTGCG 1155
                                                                                                                                                                                                                                                      1156 ATGCAAAGACTACAGCAGAACTTCTAGATCTTGCACTTGCTGATATTAATCATCAAAATT 1215
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
  Length 458;
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/organism="Lycopersicon pennellii"
/db_xref="taxon:28526"
/clone="CLPT7013"
Score 179.6; DB 9;
                                         165;
                   Pred. No. 3e-29;
                                         0; Mismatches
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AW399343.1 GI:6917813
8.3%;
62.8%;
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                                         278; Conservative
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AW399343
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/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; Leaves of various stages were shaken in liquid
nitrogen, shearing off trichomes. This procedure yielded a
mixture of cells highly enriched for trichomes, with minor
contamination by other types of leaf cells."
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                                                                                                                                                                                                             1041 AGGATACATAGGGCATTGGATTCTGATGATGTTGAATTACTACAAATGTTGCTAAGAGAG 1100
                                                                                                                                                                                                                                                                                  1101 GGGCATACTACCCTAGATGATGCATATGCTCTCCATTATGCTGTAGCGTATTGCGATGCA 1160
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                                                                                                                                                                                                                                                                                                    2 AGGATATACAAGGCATTGGATTCGGATGATGTTGAACTTGTCAAGCTTTTACTTAATGAG
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                                                                                                                                                                             ó
                                                                                                                                          Length 450;
                                                                                                                                                                             Indels
                                                                                                                                       Score 171.8; DB 9;
Pred. No. 1.6e-27;
0; Mismatches 172;
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                                                                                                                                          Similarity 61.5%; 5; Conservative (
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Job time: 1710.05 secs
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Best Local S
Matches 275
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ORIGIN
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